

From: Chan, Christina
Sent: Wednesday, April 17, 2002 3:51 PM
To: Yu, Misook; STIC-Biotech/ChemLib
Subject: RE: Rush search for 09/499,662

Please rush. Thanks Chris

-----Original Message-----

From: Yu, Misook
Sent: Wednesday, April 17, 2002 3:39 PM
To: Chan, Christina; STIC-Biotech/ChemLib
Subject: Rush search for 09/499,662

The case is due this bi-week. Would you please approve rush search for SEQID No:107 and 117? Thank you.

Examiner Misook Yu, Ph.D.
703-308-2454 (Phone)
Art Unit 1642
CM1-8E18 (Room)
CM1-8E12 (Mail Box)

RECEIVED
APR 17 2002
STIC

Point of Contact:
Barb O'Bryen
Technical Information Specialist
STIC CM1 6A05 308-4291

Searcher: BPB
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: 4-18-02
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST(where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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Result No.	Score	Query Match	Length	DB ID	Description
1	1242	100.0	238	19 AAW83034	Anti-Pas humanised
2	1242	100.0	238	21 AAB14777	Humanised anti-Pas
3	1242	100.0	238	21 AAW90927	Humanised HFE7A de
4	1230	99.0	238	19 AAW83031	Anti-Pas humanised
5	1230	99.0	238	21 AAB14772	Humanised anti-Pas
6	1230	99.0	238	21 AAW90922	Humanised anti-Pas
7	1207	97.2	238	19 AAW83035	Anti-Pas humanised
8	1207	97.2	238	21 AAB14778	Humanised anti-Pas
9	1207	97.2	238	21 AAW90928	Humanised HFE7A de
10	1201	96.7	238	19 AAW83032	Anti-Pas humanised
11	1201	96.7	238	21 AAB14773	Humanised anti-Pas

QY 1 METDILLWVLLWVPGSTGEIVLTQSPGTLISLSPGERATLSCSKASQSDYDGDSDSYMMWY 60
 Db 1 metdillwvllwvpgstgeivltqspgtlslspgeratlsckasqsgvdygdsgymwv 60
 QY 61 QOKPCQAPRLIYAASNLESIGIPDRFSGSGCTDFTLTISRLEPEDFAVYTCQOSNEDPR 120
 Db 61 qkpgqaprllyaaasnlesigipdrfsgsgctdftltisrlepfdavyytcqosnedpr 120
 QY 121 TFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCVLLNNFYPREAKVQKVDNALQ 180
 Db 121 tfgggtkleikrtvaapsvfifppsqdeqlksgtasvvcvllnnfypreakvqkvdnalqs 180
 QY 181 GNSQSVTEQDSKSTYSLSSTLTLSKADYKHKYACEVTHQGLSSPVTXSNRGE 238
 Db 181 gnsqsvteqdsksdyslsstltlskadyekhkyacevthqglsspvtksfnrgec 238

RESULT 3

AAW90927
 ID AAW90927 standard; Protein: 238 AA.

AC AAW90927;

XX 08-AUG-2000 (first entry)

DE Humanised HFE7A designed light chain protein.

XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;
 KW dermatological; immunosuppressive; thymometric; antirheumatic; anti-Fas;
 KW nephrotropic; antinfertility; neuroprotective; antiarteriosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjogren's syndrome; anemia; Addison's disease; sterility; myasthenia gravis;
 KW Goodpasture syndrome; Crohn's disease; scleroderma; sterility;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocardiitis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 XX Synthetic.

OS EP990663-A2.

PN 05-APR-2000.

XX 29-SEP-1999; 99EP-0307711.

XX 30-SEP-1998; 98JP-0276881.

PR 30-SEP-1998; 98JP-0276882.

XX (SANY) SANKYO CO LTD.

PA Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 PI WPI: 2000-258930/23.

XX N-PSDB: AAL1614.

XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
 FT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems

PS Claim 3; Page 141-142; 263pp; English.

XX This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiac and hepatotropic activity. (I) induce

CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Sjogren's disease, rheumatoid arthritis, graft
 CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody HFE7A designed light chain which is used in
 CC the method described in the invention.

XX Sequence 238 AA;

Query Match 100.0%; Score 1242; DB 21; Length 238;
 Best Local Similarity 100.0%; Pred. No. 2.9e-68;
 Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METDILLWVLLWVPGSTGEIVLTQSPGTLISLSPGERATLSCSKASQSDYDGDSDSYMMWY 60
 Db 1 metdillwvllwvpgstgeivltqspgtlslspgeratlsckasqsgvdygdsgymwv 60
 QY 61 QOKPCQAPRLIYAASNLESIGIPDRFSGSGCTDFTLTISRLEPEDFAVYTCQOSNEDPR 120
 Db 61 qkpgqaprllyaaasnlesigipdrfsgsgctdftltisrlepfdavyytcqosnedpr 120
 QY 121 TFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCVLLNNFYPREAKVQKVDNALQ 180
 Db 121 tfgggtkleikrtvaapsvfifppsqdeqlksgtasvvcvllnnfypreakvqkvdnalqs 180
 QY 181 GNSQSVTEQDSKSTYSLSSTLTLSKADYKHKYACEVTHQGLSSPVTXSNRGE 238
 Db 181 gnsqsvteqdsksdyslsstltlskadyekhkyacevthqglsspvtksfnrgec 238

RESULT 4

AAW83031
 ID AAW83031 standard; Protein: 238 AA.

AC AAW83031;

XX 15-MAR-1999 (first entry)

DE Anti-Fas humanised antibody HFE7A light chain HH type.

XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
 KW apoptosis; autoimmune disease; Hashimoto's disease;
 KW systemic lupus erythematosus; graft versus host disease;
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 KW transplant rejection; therapy.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT Peptide 1..20

FT Protein 21..238

FT /label= sig_peptide

FT /label= Mat_protein

FT Region 21..131
 FT /label= Variable
 FT Region 132..238
 FT /label= Constant
 FT Region 44..58
 FT /label= CDR_L1
 FT /note= "Claim 9"
 FT Region 74..80
 FT /label= CDR_L2
 FT /note= "Claim 9"
 FT Region 113..121
 FT /label= CDR_L3
 FT /note= "Claim 9"
 XX AU9859701-A.
 PD 08-OCT-1998.
 XX 30-MAR-1998; 98AU-0059701.
 XX 08-OCT-1997; 97JP-0276064.
 PR 01-APR-1997; 97JP-0082953.
 PR 25-JUN-1997; 97JP-0169088.
 XX (SANY) SANKYO CO LTD.
 PA Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
 XX WPI: 1998-543440/47.
 DR N-PSDB; AN70074.
 XX New antibodies and proteins bind conserved epitope of Fas antigen -
 PT used to evaluate drugs in animal models and to treat Fas-associated
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 PT myocarditis, hepatitis and AIDS
 XX Claim 21; Page 199-199; 292pp; English.
 PS This is the amino acid sequence of the HH type humanised light
 CC chain of murine anti-human Fas monoclonal antibody HFE7A.
 CC Humanisation of the murine sequence (see AAW83042) entailed making
 CC P47A, K49R, H80S, P81R, V82L, E84P, E85A, A87F and T89V amino acid
 CC substitutions; these residues are conserved in the human light
 CC chain (kappa chain). Host cell Escherichia coli PHSGH7 SANK 73497
 CC harbors plasmid PHSGH7 carrying a fusion fragment of the humanised
 CC HH type HFE7A light chain and DNA encoding the region of human
 CC immunoglobulin kappa chain, and is deposited as FERM BP-6073
 CC (claimed). The invention provides methods for producing humanised
 CC antibodies by culturing host cells. Humanised versions of HFE7A
 CC (see AAW83031-37), like native HFE7A, are capable of inducing
 CC apoptosis in abnormal cells expressing Fas, and of inhibiting
 CC Fas-induced apoptosis in normal cells. The humanised antibodies
 CC are used to evaluate, in animal models, treatments of diseases that
 CC involve Fas/Fas ligand interactions, and also to treat such
 CC diseases, including autoimmune disease (e.g. systemic lupus
 CC erythematosus, Hashimoto's disease, graft versus host disease,
 CC Sjogren syndrome, pernicious anaemia, Addison's disease,
 CC scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid
 CC arthritis, autoimmune haemolytic anaemia, sterility, myasthenia
 CC gravis, multiple sclerosis, Basedow's disease, thrombocytopenic purpura
 CC and insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
 CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
 CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).
 XX Sequence 238 AA;
 SQ
 Query Match 99.0%; Score 1230; DB 19; Length 238;
 Best Local Similarity 98.7%; Pred. NO. 1.6e-67;
 Matches 235; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1.METDTILLWVPGSGEIVLTQSPGTLSLSPGERATLSCASQSDVDYDGSYNNWY 60

Db 1 metdtillwvpgsgedivltqspgtislsgeratlsckasqsdvdydgsynnwy 60
 QY 61 QOKPGQAPRLIIYAASNLSEGIPIPRFSGSGGTDFTTISRLEPEDFAVYYCQOSNEDPR 120
 Db 61 qokpgqaprlIIyaasnllesgipdrfsgsggtDfttISRlepadfavyycqgsnedpr 120
 QY 121 TFGOGTKLEIKRTVAAPSVFIFFPPSDEQLKSGTASVYVCLLNNEYPREAKVQWQVYDNLQ 180
 Db 121 tfgggtrleikrtvaapsvfifppsdeqlksgtasvvcvllnnfypreakvqwkvdnlqs 180
 QY 181 GNSQESVTEQDSKDSYSLSTLTLSKADYEKHVYACEVTHQGLSPVTKSFNRGEC 238
 Db 181 gnsqesvteqdsksdystltskadyekhkvyacevthqglsspvtksfnrgec 238
 RESULT 5
 AAB14772
 ID AAB14772 standard; Protein: 238 AA.
 XX
 AC AAB14772;
 XX
 DT 24-NOV-2000 (first entry)
 XX
 DE Humanised anti-Fas antibody light chain, SEQ ID NO:50.
 XX
 KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-Bp-5828;
 KW murine; humanised antibody; complementarity determining region; CDR;
 KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;
 KW hepatitis; AIDS; graft rejection; light chain.
 XX
 OS Chimeric - Mus musculus.
 OS Chimeric - Homo sapiens.
 XX
 PN JP2000169393-A.
 XX
 PD 20-JUN-2000.
 XX
 PF 30-SEP-1999; 99JP-0278301.
 XX
 PR 30-SEP-1998; 98JP-0276883.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 DR WPI: 2000-485645/43.
 DR N-PSDB; AAW72124.
 XX
 PT Preventive or treating agent for the diseases caused by an abnormality
 PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains
 PT anti-Fas antibody -
 XX
 PS Claim 20; Page 78-79; 139pp; Japanese.
 XX
 CC The invention relates to compositions for the prevention or treatment
 CC of diseases caused by an abnormality in the Fas/Fas ligand system
 CC containing an anti-Fas antibody as the active component. The anti-Fas
 CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
 CC or a humanised version of HFE7A containing identical CDRs
 CC (complementarity determining regions) to antibody HFE7A. Via its
 CC interaction with Fas, the antibody of the invention acts as a modulator
 CC of apoptosis. The composition of the invention may therefore be used in
 CC the treatment or prevention of conditions such as autoimmune diseases,
 CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
 CC glomerulonephritis, aplastic anaemia (pancytopenia), hepatitis, AIDS
 CC and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778
 CC represent the light chains of several humanised HFE7A-derived anti-Fas
 CC antibodies.
 XX
 SQ Sequence 238 AA;

Query Match 99.0%; Score 1230; DB 21; Length 238;
 Best Local Similarity 98.7%; Pred. No. 1.6e-67;
 Matches 235; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 METDTILLWLLWVPGSTGEIVLTQSPGTLSPGERATLSCSKASQSDYDGSYMNWY 60
 DB 1 metdtillwllwvpgstgdvltqspgtlslspgeratlsckasqsdvdydgsymnw 60

QY 61 QORPGQAPRLIIYAASNLSEIGIPDRFSGSGGTDTFTLTISRLEPEDFAVYQCQSNEDPR 120
 DB 61 qkpgqaprrlliyaasnlseigipdrfsgsggttdftltisrlepadvavycqsgnedpr 120

QY 121 TFGOGTLEIKRTVAAPSVFPPSDQLKSGTASVVCVLLNFPREAKVQWKVDNALQS 180
 DB 121 tfgogtgleikrtvaapsvfppsdqklsgtasvvcvllnfpreakvqwkvdnalqs 180

QY 181 GNSQESVTEQDSKDSYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
 DB 181 gnsqesvteqdsksdystlslstltlskadyekhkvacevthqglsspvtksfnrgec 238

RESULT 6
 AAW90922 ID AAW90922 standard; Protein; 238 AA.
 AC AAW90922;
 DT 08-AUG-2000 (first entry)
 XX Humanised anti-Fas antibody HFE7A light chain HH type protein.

Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 dermatological; immunosuppressive; thyromimetic; antineuritic; anti-Fas;
 nephrotropic; antinfertility; neuroprotective; antineuritic; anti-Fas;
 hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;
 Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 Synthetic.

EP909663-A2.
 05-APR-2000.
 29-SEP-1999; 99EP-0307711.
 30-SEP-1998; 98JP-0276881.
 30-SEP-1998; 98JP-0276882.
 (SANY) SANKYO CO LTD.
 Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 WPI: 2000-258930/23.
 N-PSDB; AAA11562.

New humanized anti-Fas antibody, useful for treating or preventing e.g.
 inflammatory or autoimmune disease, induces apoptosis selectively in
 cells with abnormal Fas-Fas ligand systems -
 Example reference 14; Page 114-115; 263pp; English.

This invention describes a novel humanized anti-Fas antibody-like
 molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 ligand system, by binding to Fas on the cell surface, and prevents
 apoptosis in cells with a normal system, by inhibiting binding between
 Fas and its ligand. The products of the invention have anti-inflammatory,
 anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,

CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody HFE7A light chain HH type which is used in
 CC the method described in the invention.

XX
 SQ Sequence 238 AA;

Query Match 99.0%; Score 1230; DB 21; Length 238;
 Best Local Similarity 98.7%; Pred. No. 1.6e-67;
 Matches 235; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 METDTILLWLLWVPGSTGEIVLTQSPGTLSPGERATLSCSKASQSDYDGSYMNWY 60
 DB 1 metdtillwllwvpgstgdvltqspgtlslspgeratlsckasqsdvdydgsymnw 60

QY 61 QORPGQAPRLIIYAASNLSEIGIPDRFSGSGGTDTFTLTISRLEPEDFAVYQCQSNEDPR 120
 DB 61 qkpgqaprrlliyaasnlseigipdrfsgsggttdftltisrlepadvavycqsgnedpr 120

QY 121 TFGOGTLEIKRTVAAPSVFPPSDQLKSGTASVVCVLLNFPREAKVQWKVDNALQS 180
 DB 121 tfgogtgleikrtvaapsvfppsdqklsgtasvvcvllnfpreakvqwkvdnalqs 180

QY 181 GNSQESVTEQDSKDSYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
 DB 181 gnsqesvteqdsksdystlslstltlskadyekhkvacevthqglsspvtksfnrgec 238

RESULT 7

AAW83035

ID AAW83035 standard; Protein; 238 AA.

AC AAW83035;

DT 15-MAR-1999 (first entry)

DE Anti-Fas humanised antibody HFE7A light chain PDHM type.

XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
 KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
 KW systemic lupus erythematosus; graft versus host disease;
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 KW transplant rejection; therapy.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FH Key 1..20

FT Peptide

FT Protein /label= Sig_peptide
 FT 21..238
 FT /label= Mat_protein
 FT 21..131
 FT /label= Variable
 FT 132..238
 FT /label= Constant
 FT 44..58
 FT /note= "claim 9"
 FT 74..80
 FT /label= CDR_L1
 FT /label= CDR_L2
 FT /note= "claim 9"
 FT 113..121
 FT /label= CDR_L3
 FT /note= "claim 9"
 XX AU9859701-A.
 XX
 XX 08-OCT-1998.
 XX
 XX 30-MAR-1998; 98AU-0059701.
 XX
 XX 08-OCT-1997; 97JP-0276064.
 PR 01-APR-1997; 97JP-0082953.
 PR 25-JUN-1997; 97JP-0169088.
 XX
 XX (SANY) SANKYO CO LTD.
 PA
 XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
 XX
 XX WPI; 1998-543440/47.
 DR N-PSDB; AAV70078.
 XX
 XX New antibodies and proteins bind conserved epitope of Fas antigen -
 PT used to evaluate drugs in animal models and to treat Fas-associated
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 PT myocarditis, hepatitis and AIDS
 XX
 XX Claim 21; Page 220-221; 292pp; English.
 PS
 XX
 XX This is the amino acid sequence of the PDHM type humanised light
 CC chain of murine anti-human Fas monoclonal antibody HFE7A.
 CC Humanisation of the murine sequence (see AAW83042) entailed making
 CC DiE, P47A, K49R and R107K amino acid substitutions; these
 CC residues are conserved in the human light (kappa) chain. Host
 CC cell Escherichia coli pSHM2 SANK 70198 harbors plasmid pSHM2
 CC carrying a fusion of the humanised PDHM type HFE7A light chain and
 CC DNA encoding the region of human immunoglobulin kappa chain, and is
 CC deposited as FERM BP-6272 (claimed). The invention provides
 CC methods for producing humanised antibodies by culturing host
 CC cells. Humanised versions of HFE7A (see AAW83031-37), like native
 CC HFE7A, are capable of inducing apoptosis in abnormal cells
 CC expressing Fas, and of inhibiting Fas-induced apoptosis in normal
 CC cells. The humanised antibodies are used to evaluate, in animal
 CC models, treatments of diseases that involve Fas/Fas ligand
 CC interactions, and also to treat such diseases, including autoimmune
 CC disease (e.g. systemic lupus erythematosus, Hashimoto's disease,
 CC graft versus host disease, Sjogren syndrome, pernicious anaemia,
 CC Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, rheumatoid arthritis, autoimmune haemolytic anaemia,
 CC sterility, myasthenia gravis, multiple sclerosis, Basedow's disease,
 CC thrombopenia purpura and insulin-dependent diabetes), allergies,
 CC atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
 CC nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant
 CC rejection (all claimed).
 XX
 XX Sequence 238 AA;

Query Match 97.2%; Score 1207; DB 19; Length 238;
 Best Local Similarity 97.5%; Pred. No. 3.8e-66;

Matches 232; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 1 METDTILLWLLWVPGSTGEIVLTQSPGTLSLSPGERATLSCCKASQSYVDYDGSYNNWY 60
 DB 1 metdtillwvllwvpstgeivltspgtlslspgeratlsckasqsyvdgdsymnw 60
 QY 61 QKPGQAPRLIIYAASNLSEGPIDRFSGSGGTDFLTITISRLPEPEFAYVYCOQSNEDPR 120
 DB 61 qkpgqaprllyaaaslesgipdrfsgsgsgtdftltihpveedaatyycqgsnedpr 120
 QY 121 TFCQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRKAVQWVKVNDALQS 180
 DB 121 tfgggtkileikrtvaapsvfifppsdeqlksgtasvvcllnnfyprkavqwkvdnals 180
 QY 181 GNSQESVTEQDSKDSYSLSTLTLSKADYKHKVACEVTHOGLSSPVTKSNRGEC 238
 DB 181 gnsqesvteqdsksdyslssltsltlskadyekhkvyacevthdgslsspvcksnrgec 238
 RESULT 8
 AAB14778
 ID AAB14778 standard; Protein; 238 AA.
 XX
 XX AAB14778;
 XX
 XX 24-NOV-2000 (first entry)
 XX
 XX Humanised anti-Fas antibody light chain, SEQ ID NO:109.
 XX
 XX Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
 KW murine; humanised antibody; complementarity determining region; CDR;
 KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;
 KW hepatitis; AIDS; graft rejection; light chain.
 XX
 XX Chimeric - Mus musculus.
 OS Chimeric - Homo sapiens.
 XX
 XX JP2000169393-A.
 XX
 XX 20-JUN-2000.
 XX
 XX 30-SEP-1999; 95JP-0278301.
 XX
 XX 30-SEP-1998; 98JP-0276883.
 XX
 XX (SANY) SANKYO CO LTD.
 XX
 XX WPI; 2000-485645/43.
 DR N-PSDB; AAA72177.
 XX
 XX Preventive or treating agent for the diseases caused by an abnormality
 PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains
 PT anti-Fas antibody -
 XX
 XX Claim 20; Page 103; 139pp; Japanese.
 XX
 XX The invention relates to compositions for the prevention or treatment
 CC of diseases caused by an abnormality in the Fas/Fas ligand system
 CC containing an anti-Fas antibody as the active component. The anti-Fas
 CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
 CC or a humanised version of HFE7A containing identical CDRs
 CC (complementarity determining regions) to antibody HFE7A. Via its
 CC interaction with Fas, the antibody of the invention acts as a modulator
 CC of apoptosis. The compositions of the invention may therefore be used in
 CC the treatment or prevention of conditions such as autoimmune diseases,
 CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
 CC and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778
 CC represent the light chains of several humanised HFE7A-derived anti-Fas
 CC antibodies.
 XX

SQ Sequence 238 AA;

Query Match 97.2%; Score 1207; DB 21; Length 238;
 Best Local Similarity 97.5%; Pred. No. 3.8e-66;
 Matches 232; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 METDTILLWVLLWVPGSTGEIVLTQSPGTLSLSPGERATLSCRSQSDVDYDGSYNNWY 60
 DB 1 metdtillwvllwvpgstgeivltqspgtlsispggeratlsckasgsdvydgsymnw 60

QY 61 QOKPQAPRLIYAASNLSEGIPIRFSGSGTDTLTISLEPEDFAVYCCQSNEDPR 120
 DB 61 qkpgqaprllyaaasnlsegiipdrfsgsgtdtltihpveedaatyccgsnedpr 120

QY 121 TFGOGTKLEIKRTVAAPSVFIPTSPDQLSGTASVCLLNFFTPRAKQVQKVDNALQS 180
 DB 121 tfgogtkleikrtvaapsvfippsdqlsgtasvcllnfftpreakvqkvdnalqs 180

QY 181 GNSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
 DB 181 gnsqesvteqdsksdystlslstltlskadyekhkvyacevthqglsspvtksfnrgec 238

RESULT 9
 AAW90928
 ID AAW90928 standard; Protein; 238 AA.
 AC AAW90928;
 DT 08-AUG-2000 (first entry)
 DE Humanised HFE7A designed light chain protein #2.

Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;
 dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
 hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 Sjogren's syndrome; Addison's disease; scleroderma; sterility;
 Goodpasture syndrome; Crohn's disease; thrombopenia purpura; allergy;
 multiple sclerosis; Basedow's disease; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 insulin dependent diabetes mellitus; hepatitis; transplant rejection.
 cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 Synthetic.

EP990663-A2.
 05-APR-2000.
 29-SEP-1999; 99EP-0307711.
 30-SEP-1998; 98JP-0276881.
 30-SEP-1998; 98JP-0276882.
 (SANY) SANKYO CO LTD.
 Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 WPT; 2000-258930/23.
 N-PSDB; AAA11615.

New humanized anti-Fas antibody, useful for treating or preventing e.g.
 inflammatory or autoimmune disease, induces apoptosis selectively in
 cells with abnormal Fas-Fas ligand systems

Example reference 21; Page 144-145; 263pp; English.

This invention describes a novel humanized anti-Fas antibody-like
 molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 ligand system, by binding to Fas on the cell surface, and prevents

CC apoptosis in cells with a normal system, by inhibiting binding between
 Fas and its ligand. The products of the invention have anti-inflammatory,
 anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 antirheumatic, nephrotropic, antiinfertility, neuroprotective,
 antiarteriosclerotic, cardiac and hepatotropic activity. (I) induce
 apoptosis by binding to cell surface Fas or inhibit it by competitive
 inhibition of ligand binding. (I) are used to treat and/or prevent
 diseases associated with the Fas/Fas ligand system, especially systemic
 lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 versus host disease, Sjogren's syndrome, pernicious or hypoplastic
 anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 (B, C or D) alcoholic), and transplant rejection. (I) selectively
 inhibit apoptosis in normal cells but selectively induce it in abnormal
 cells. They bind to both human and murine Fas, so can be evaluated in
 murine disease models. (I) act on the active site of Fas, i.e. they mimic
 the native ligand, do not induce liver disease, and have reduced risk of
 inducing a human anti-murine antibody response. This sequence represents
 a humanised anti-Fas antibody HFE7A designed light chain which is used in
 the method described in the invention.

XX SQ Sequence 238 AA;

Query Match 97.2%; Score 1207; DB 21; Length 238;
 Best Local Similarity 97.5%; Pred. No. 3.8e-66;
 Matches 232; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 METDTILLWVLLWVPGSTGEIVLTQSPGTLSLSPGERATLSCRSQSDVDYDGSYNNWY 60
 DB 1 metdtillwvllwvpgstgeivltqspgtlsispggeratlsckasgsdvydgsymnw 60

QY 61 QOKPQAPRLIYAASNLSEGIPIRFSGSGTDTLTISLEPEDFAVYCCQSNEDPR 120
 DB 61 qkpgqaprllyaaasnlsegiipdrfsgsgtdtltihpveedaatyccgsnedpr 120

QY 121 TFGOGTKLEIKRTVAAPSVFIPTSPDQLSGTASVCLLNFFTPRAKQVQKVDNALQS 180
 DB 121 tfgogtkleikrtvaapsvfippsdqlsgtasvcllnfftpreakvqkvdnalqs 180

QY 181 GNSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
 DB 181 gnsqesvteqdsksdystlslstltlskadyekhkvyacevthqglsspvtksfnrgec 238

RESULT 10
 AAW83032
 ID AAW83032 standard; Protein; 238 AA.
 AC AAW83032;
 DT 15-MAR-1999 (first entry)
 DE Anti-Fas humanised antibody HFE7A light chain HM type.
 XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
 XX apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
 XX systemic lupus erythematosus; graft versus host disease;
 XX Sjogren syndrome; pernicious anaemia; Addison's disease;
 XX scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 XX rheumatoid arthritis; autoimmune haemolytic anaemia;
 XX myasthenia gravis; multiple sclerosis; Basedow's disease;
 XX thrombopenia purpura; insulin-dependent diabetes; allergy;
 XX atopy; arteriosclerosis; myocarditis; cardiomyopathy;
 XX glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 XX transplant rejection; therapy.
 XX Homo sapiens.
 OS Synthetic.

XX FH Key Location/Qualifiers
 FT Peptide 1..20
 FT Protein /label= Sig_peptide
 FT 21..238
 FT Region /label= Mat_protein
 FT 21..131
 FT Region /label= Variable
 FT 132..238
 FT Region /label= Constant
 FT 44..58
 FT Region /label= CDR_L1
 FT /note= "Claim 9"
 FT 74..80
 FT Region /label= CDR_L2
 FT /note= "Claim 9"
 FT 113..121
 FT Region /label= CDR_L3
 FT /note= "Claim 9"
 XX AU9859701-A.
 XX
 XX 08-OCT-1998.
 XX
 XX 30-MAR-1998; 98AU-0059701.
 XX
 XX 08-OCT-1997; 97JP-0276064.
 XX 01-APR-1997; 97JP-0082953.
 XX 25-JUN-1997; 97JP-0169088.
 XX
 XX (SANY) SANKYO CO LTD.
 XX
 XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
 XX
 XX WPI: 1998-543440/47.
 DR N-PSDB; AA70075.
 DR
 DR
 DR
 XX New antibodies and proteins bind conserved epitope of Fas antigen -
 XX used to evaluate drugs in animal models and to treat Fas-associated
 XX diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 XX myocarditis, hepatitis and AIDS
 XX
 XX Claim 21; Page 200; 292pp; English.
 PS
 XX
 XX This is the amino acid sequence of the HM type humanised light
 CC chain of murine anti-human Fas monoclonal antibody HFE7A.
 CC Humanisation of the murine sequence (see AA83042) entailed making
 CC P47A and K49R amino acid substitutions; these residues are
 CC conserved in the human light (kappa) chain. Host cell E. coli
 CC PHSGHM17 SANK 73597 harbors plasmid PHSGHM17 carrying a fusion
 CC fragment of the humanised HM type HFE7A light chain and DNA
 CC encoding the region of human immunoglobulin kappa chain, and is
 CC deposited as FERM BP-6072 (claimed). The invention provides
 CC methods for producing humanised antibodies by culturing host
 CC cells. Humanised versions of HFE7A (see AA83031-37), like native
 CC HFE7A, are capable of inducing apoptosis in abnormal cells
 CC expressing Fas, and of inhibiting Fas-induced apoptosis in normal
 CC cells. The humanised antibodies are used to evaluate, in animal
 CC models, treatments of diseases that involve Fas/Fas ligand
 CC interactions, and also to treat such diseases, including autoimmune
 CC disease (e.g. systemic lupus erythematosus, Hashimoto's disease,
 CC graft versus host disease, Sjogren syndrome, pernicious anaemia,
 CC Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, rheumatoid arthritis, autoimmune haemolytic anaemia,
 CC sterility, myasthenia gravis, multiple sclerosis, Basedow's disease,
 CC thrombopenia purpura and insulin-dependent diabetes), allergies,
 CC atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
 CC nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant
 CC rejection (all claimed).
 XX
 XX Sequence 238 AA;

Query Match 96.7%; Score 1201; DB 19; Length 238;
 Best Local Similarity 96.6%; Pred. No. 8.9e-66;
 Matches 230; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 QY 1 METDTILLWVLLWVPGSTGEIVLTQSPGTLSLSPGERATLSCASQSVYDGDSYNNY 60
 DB 1 metdtillwvllwvpgstgdvltqspgtlsispggeratlscaskasvdygdgsmyny 60
 QY 61 QQKPGQAPRLIYAASNLESGIPDRFSGSGTDFTLTISRLEPEDFAVYVCOOSNEDPR 120
 DB 61 qqkpgqaprllyaaasnielesgipdrfsgsgtdftltihpveeedaatyyccqsnedpr 120
 QY 121 TFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRRAKYVQWYVDNALQS 180
 DB 121 tfgggtlrleikrtvaapsvfifppsdeqlksgtasvcllnnfyprreakyqwkvdnalqs 180
 QY 181 GNSQESVTEQDSKDSYSLSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSNRGEC 238
 DB 181 gnsqesvteqdkdstyslsstltlskadyekkhvacevthgglsspvtksnrgec 238
 RESULT 11
 AABI4773
 ID AABI4773 standard; Protein; 238 AA.
 XX
 XX AC AABI4773;
 XX
 XX DT 24-NOV-2000 (first entry)
 XX
 XX DE Humanised anti-Fas antibody light chain, SEQ ID NO:52.
 XX
 KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
 KW murine; humanised antibody; complementarity determining region; CDR;
 KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pannyelophthisis;
 KW hepatitis; AIDS; graft rejection; light chain.
 XX
 OS Chimeric - Mus musculus.
 OS Chimeric - Homo sapiens.
 XX
 XX PN JP2000169393-A.
 XX
 XX PD 20-JUN-2000.
 XX
 XX PF 30-SEP-1999; 99JP-0278301.
 XX
 XX PR 30-SEP-1998; 98JP-0276883.
 XX
 XX PA (SANY) SANKYO CO LTD.
 XX
 XX DR WPI: 2000-485645/43.
 XX DR N-PSDB; AA72125.
 XX
 XX PT Preventive or treating agent for the diseases caused by an abnormality
 XX in the Fas/Fas ligand system e.g. autoimmune diseases, contains
 XX anti-Fas antibody
 XX
 XX PS Claim 20; Page 80-81; 139pp; Japanese.
 XX
 CC The invention relates to compositions for the prevention or treatment
 CC or diseases caused by an abnormality in the Fas/Fas ligand system
 CC containing an anti-Fas antibody as the active component. The anti-Fas
 CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
 CC or a humanised version of HFE7A containing identical CDRs
 CC (complementarity determining regions) to antibody HFE7A. Via its
 CC interaction with Fas, the antibody of the invention acts as a modulator
 CC of apoptosis. The compositions of the invention may therefore be used in
 CC the treatment or prevention of conditions such as autoimmune diseases,
 CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
 CC and organ graft rejection. Sequences AABI4772-B14774 and AABI4777-B14778

CC represent the light chains of several humanised HFE7A-derived anti-Fas
 CC antibodies.

XX Sequence 238 AA;

Query Match 96.7%; Score 1201; DB 21; Length 238;
 Best Local Similarity 96.6%; Pred. No. 8.9e-66;
 Matches 230; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 METDTILLWLLVPGSTGEIVLTQSPGTLSPGERATLSCSKASQSDYDGDSPYNNWY 60
 |||||
 Db 1 metdtillwllwpvgstgdivltqspgtlslspgeratlsckasgsvdydgdsymnw 60
 QY 61 QQRPGQAPRLIIYAASNLGSGIPDRFSGSGGTDTLTISRLEPEDFAVYTCQSNEDPR 120
 |||||
 Db 61 qkpgqgprlliyaasnlsgipdrfsgsggtgdtltihpveeadaatyccqgsnedpr 120
 QY 121 TFGOGTLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
 |||||
 Db 121 tfgogtltreikrtvaapsvfifppsdgklsqgtasvvcvllnnfypreakvqwkvdnals 180
 QY 181 GNSQESVTEQDQSDYSTLSSTLTSLKADYKHKVYACEVTHQGLSPVTKSFNRGEC 238
 |||||
 Db 181 gnsqesvteqgskdstyslsstltlskadyekhkvyacevthqglspvcksfnrgec 238

RESULT 12

AAW90923

ID AAW90923 standard; Protein; 238 AA.

XX AAW90923;

XX 08-AUG-2000 (first entry)

XX Humanised anti-Fas antibody HFE7A light chain HM type protein.

XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 XX anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 XX dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 XX nephrotropic; antinfertility; neuroprotective; antiarteriosclerotic;
 XX hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 XX Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 XX Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;
 XX Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 XX multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 XX insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 XX cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

XX Synthetic.

XX EP990663-A2.

XX 05-APR-2000.

XX 29-SEP-1999; 99EP-0307711.

XX 30-SEP-1998; 98JP-0276881.

XX 30-SEP-1998; 98JP-0276882.

XX (SANY) SANKYO CO LTD.

XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;

XX WPI; 2000-258930/23.

XX N-PSDB; AAA11563.

XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems

XX Example reference 14; Page 117-118; 263pp; English.

XX

CC This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody HFE7A light chain HM type which is used in
 CC the method described in the invention.

XX Sequence 238 AA;

Query Match 96.7%; Score 1201; DB 21; Length 238;
 Best Local Similarity 96.6%; Pred. No. 8.9e-66;
 Matches 230; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 METDTILLWLLVPGSTGEIVLTQSPGTLSPGERATLSCSKASQSDYDGDSPYNNWY 60
 |||||

Db 1 metdtillwllwpvgstgdivltqspgtlslspgeratlsckasgsvdydgdsymnw 60
 |||||

QY 61 QQRPGQAPRLIIYAASNLGSGIPDRFSGSGGTDTLTISRLEPEDFAVYTCQSNEDPR 120
 |||||

Db 61 qkpgqgprlliyaasnlsgipdrfsgsggtgdtltihpveeadaatyccqgsnedpr 120
 |||||

QY 121 TFGOGTLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
 |||||

Db 121 tfgogtltreikrtvaapsvfifppsdgklsqgtasvvcvllnnfypreakvqwkvdnals 180
 |||||

QY 181 GNSQESVTEQDQSDYSTLSSTLTSLKADYKHKVYACEVTHQGLSPVTKSFNRGEC 238
 |||||

Db 181 gnsqesvteqgskdstyslsstltlskadyekhkvyacevthqglspvcksfnrgec 238
 |||||

RESULT 13

AAW83033

ID AAW83033 standard; Protein; 238 AA.

XX AAW83033;

XX 15-MAR-1999 (first entry)

XX Anti-Fas humanised antibody HFE7A light chain MM type.

XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
 XX apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
 XX systemic lupus erythematosus; graft versus host disease;
 XX Sjogren syndrome; pernicious anaemia; Addison's disease;
 XX scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 XX rheumatoid arthritis; autoimmune haemolytic anaemia;
 XX myasthenia gravis; multiple sclerosis; Basedow's disease;
 XX thrombopenia purpura; insulin-dependent diabetes; allergy;
 XX atopy; arteriosclerosis; myocarditis; cardiomyopathy;
 XX glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 XX transplant rejection; therapy.

XX Homo sapiens.
OS Synthetic.
XX

XX Key Location/Qualifiers
FT Peptide 1..20
FT /label= Sig_peptide
FT Protein 21..238
FT /label= Mat_protein
FT Region 21..131
FT /label= Variable
FT Region 132..238
FT /label= Constant
FT Region 44..58
FT /label= CDR_L1
FT /note= "claim 9"
FT Region 74..80
FT /label= CDR_L2
FT /note= "claim 9"
FT Region 113..121
FT /label= CDR_L3
FT /note= "claim 9"

XX AU9859701-A.
XX
XX 08-OCT-1998.
XX
XX 30-MAR-1998; 98AU-0059701.
XX
XX 08-OCT-1997; 97JP-0276064.
XX 01-APR-1997; 97JP-0082953.
XX 25-JUN-1997; 97JP-0169088.
XX
XX (SANY) SANKYO CO LTD.
XX
XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
XX Masahiko O, Nobufusa S, Shin Y, Tohru T;
XX
XX WPI; 1998-543440/47.
XX N-PSDB; AAV70076.
XX
XX New antibodies and proteins bind conserved epitope of Fas antigen -
XX used to evaluate drugs in animal models and to treat Fas-associated
XX diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
XX myocarditis, hepatitis and AIDS
XX
XX Claim 21: Page 202; 292pp; English.

XX This is the amino acid sequence of the MM type humanised light
XX chain of murine anti-human Fas monoclonal antibody HFE7A. E. coli
XX SANK 73697 harbors plasmid pHSMM6 carrying a fusion fragment of the
XX humanised MM type HFE7A light chain and DNA encoding the region of
XX human kappa chain, and is deposited as FERM BP-6071 (claimed). The
XX invention provides methods for producing humanised antibodies by
XX culturing host cells. Humanised versions of HFE7A (see AAW83031-37),
XX like native HFE7A, are capable of inducing apoptosis in abnormal
XX cells expressing Fas, and of inhibiting Fas-induced apoptosis in
XX normal cells. The humanised antibodies are used to evaluate, in
XX animal models, treatments of diseases that involve Fas/Fas ligand
XX interactions, and also to treat such diseases, including autoimmune
XX disease (e.g. systemic lupus erythematosus, Hashimoto's disease,
XX graft versus host disease, Sjogren syndrome, pernicious anaemia,
XX Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
XX disease, rheumatoid arthritis, autoimmune haemolytic anaemia,
XX sterility, myasthenia gravis, multiple sclerosis, Basedow's disease,
XX thrombopenia purpura and insulin-dependent diabetes), allergies,
XX atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
XX nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant
XX rejection (all claimed).

XX Sequence 238 AA;

Query Match 96.1%; Score 1193; DB 19; Length 238;
Best Local Similarity 95.8%; Pred. No. 2.7e-65;
Matches 228; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 METDTILLWVPGSTGEIVLTQSPGTLSLSPGERATLSCASQSDVDGDSYMNWY 60
DB 1 metdtilwvllwvpgstgdivltqspgtlsispgeratlsckasqsdvdygdsymnw 60
QY 61 QKPGQAPRLIYAASNLESGIPDRFSGSGTDFTLTISRLEPEDFAVYVCOQSNEDPR 120
DB 61 qkpgqppklliyaasnlsgipdrfsgsgtdftltihpveedaatyycqqsndpr 120
QY 121 TFCQGTLEIKRTVAAPSVFIFPPSDQKLSGTASVVCVLLNNFYPREAKYQWKVDNALQS 180
DB 121 tfcggtrleikrtvaapsvfifppsdeqlksgtasvvcvllnnfypreakyqwkvdnalqs 180
QY 181 GNSQESVTEQDSKDSYSLSSLTLSKADYKHKVACEVTHQGLSSPVTKSNRGEC 238
DB 181 gnsqesvteqdsksdyslssltlslskadyekhkvacevthqglsspvtksnrgec 238

RESULT 14
AAB14774
ID AAB14774 standard; Protein; 238 AA.
XX AC
XX AAB14774;
XX
XX 24-NOV-2000 (first entry)
XX
XX Humanised anti-Fas antibody light chain, SEQ ID NO:54.
XX
XX Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
XX murine; humanised antibody; complementarity determining region; CDR;
XX human Fas; Fas ligand; apoptosis modulator; programmed cell death;
XX autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
XX cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;
XX hepatitis; AIDS; graft rejection; light chain.
XX
XX Chimeric - Mus musculus.
XX Chimeric - Homo sapiens.
XX
XX JP2000169393-A.
XX
XX 20-JUN-2000.
XX
XX 30-SEP-1999; 99JP-0278301.
XX
XX 30-SEP-1998; 98JP-0276883.
XX
XX (SANY) SANKYO CO LTD.
XX
XX WPI: 2000-485645/43.
XX N-PSDB; AAA72126.
XX
XX Preventive or treating agent for the diseases caused by an abnormality
XX in the Fas/Fas ligand system e.g. autoimmune diseases, contains
XX anti-Fas antibody
XX
XX Claim 20; Page 83; 139pp; Japanese.

XX The invention relates to compositions for the prevention or treatment
XX or diseases caused by an abnormality in the Fas/Fas ligand system
XX containing an anti-Fas antibody as the active component. The anti-Fas
XX antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
XX or a humanised version of HFE7A containing identical CDRs
XX (complementarity determining regions) to antibody HFE7A. Via its
XX interaction with Fas, the antibody of the invention acts as a modulator
XX of apoptosis. The composition of the invention may therefore be used in
XX the treatment or prevention of conditions such as autoimmune diseases,
XX allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
XX glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
XX and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778
XX represent the light chains of several humanised HFE7A-derived anti-Fas

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OM protein - protein search, using sw model

Run on: April 17, 2002, 16:36:57 ; Search time 21.24 Seconds
(without alignments)
252.156 Million cell updates/sec

Title: US-09-499-662-107
Perfect score: 1242
Sequence: 1 METDILLWVLLWPGSTG.....EVTHOGLSPVTKSFNRGEC 238

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
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3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1050	84.5	218	5	PCT-US96-13152-2
2	1036	83.4	218	2	US-08-887-352B-13
3	1036	83.4	218	3	US-08-466-151-9
4	1036	83.4	218	4	US-09-109-207C-13
5	1036	83.4	218	4	US-09-296-005-13
6	1013	81.6	218	4	US-09-282-505-1
7	1013	81.6	218	4	US-09-054-255-1
8	1010	81.3	218	2	US-08-887-352B-15
9	1010	81.3	218	2	US-08-887-352B-17
10	1010	81.3	218	2	US-08-887-352B-19
11	1010	81.3	218	2	US-08-887-352B-24
12	1010	81.3	218	4	US-09-109-207C-15
13	1010	81.3	218	4	US-09-109-207C-17
14	1010	81.3	218	4	US-09-109-207C-19
15	1010	81.3	218	4	US-09-109-207C-24
16	1010	81.3	218	4	US-09-296-005-15
17	1010	81.3	218	4	US-09-296-005-17
18	1010	81.3	218	4	US-09-296-005-19
19	1010	81.3	218	4	US-09-296-005-24
20	979.5	78.9	241	2	US-07-916-098A-56
21	976.5	78.6	239	3	US-08-487-550-6
22	976	78.6	234	4	US-09-049-672A-6
23	966.5	77.8	235	1	US-08-276-852-153
24	966.5	77.8	235	1	US-08-899-575-153
25	966.5	77.8	235	1	US-08-899-575-153
26	966.5	77.8	235	1	PCT-US95-08743-153
27	958.5	77.2	233	2	US-07-934-373C-25

28	958.5	77.2	233	3	US-08-437-642B-25
29	958.5	77.2	233	5	PCT-US93-07832-25
30	957.5	77.1	235	4	US-09-171-945-97
31	956.5	77.0	214	2	US-08-480-753-6
32	956.5	77.0	214	3	US-09-041-889-11
33	956.5	77.0	214	3	US-08-837-058-11
34	955	76.9	214	2	US-07-934-373C-39
35	955	76.9	214	3	US-08-437-642B-39
36	955	76.9	214	5	PCT-US93-07832-39
37	955	76.9	236	1	US-08-157-101A-5
38	950	76.5	214	2	US-07-934-373C-40
39	950	76.5	214	2	US-08-788-800-11
40	950	76.5	214	3	US-08-437-642B-40
41	950	76.5	214	3	US-09-097-309-2
42	950	76.5	214	4	US-09-097-171A-2
43	950	76.5	214	5	PCT-US93-07832-40
44	950	76.5	237	3	US-09-097-309-6
45	950	76.5	237	4	US-09-097-171A-10

ALIGNMENTS

RESULT 1
PCT-US96-13152-2
; Sequence 2, Application PC/TUS9613152
; GENERAL INFORMATION:
; APPLICANT: Martin, Ulrich, et al.
; TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ f
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; ADDRESS: Attn: Norman D. Hanson
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Computer Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/13152
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/578,953
; FILING DATE: 27-Dec-95
; APPLICATION NUMBER: EP 95 112 895.8
; FILING DATE: 17-Aug-95
; APPLICATION NUMBER: EP 95 114 969.9
; FILING DATE: 19-Sep-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Norman D. Hanson
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-13152-2

Query Match 84.5%; Score 1050; DB 5; Length 218;
Best Local Similarity 91.3%; Pred. NO. 2a-81;

QY 141 IFPPSDEQLKSGTASVYVCLLNFFPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 200
 Db 121 IFPPSDEQLKSGTASVYVCLLNFFPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180

QY 201 STLTLKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 238
 Db 181 STLTLKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 4
 US-09-109-207C-13
 ; Sequence 13, Application US/09109207C
 ; Patent No. 6172213
 ; GENERAL INFORMATION:
 ; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
 ; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
 ; FILE REFERENCE: P1123R1
 ; CURRENT APPLICATION NUMBER: US/09/109,207C
 ; CURRENT FILING DATE: 1998-06-30
 ; PRIOR APPLICATION NUMBER: US 60/051,554
 ; PRIOR FILING DATE: 1997-07-03
 ; NUMBER OF SEQ ID NOS: 44
 ; SEQ ID NO 13
 ; LENGTH: 218
 ; TYPE: PRT
 ; ORGANISM: Artificial
 ; FEATURE:
 ; NAME/KEY: Artificial
 ; LOCATION: 1-218
 ; OTHER INFORMATION: Light chain sequence derived from MAE11
 US-09-109-207C-13

Query Match 83.4%; Score 1036; DB 4; Length 218;
 Best Local Similarity 89.9%; Pred. No. 3.1e-80;
 Matches 196; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 21 EIVLTQSPGTLSPGERATLSCASQSDYDGDSDYNNWYQOKPGQAPRLIIYAASNLES 80
 Db 1 DIQLTQSPSSLSASVGDRTITCRASQSDYDGDSDYNNWYQOKPGKAPKLLIIYAASYLE 60
 QY 81 GIPDRFSGSGGTDFLTITSLRLEPEDFAVYCCQSNEDPRTFGQGTKEIKRTVAAPSVF 140
 Db 61 GVPDRFSGSGGTDFLTITSLRLEPEDFAVYCCQSHEDPYTFGGQTKVEIKRTVAAPSVF 120
 QY 141 IFPPSDEQLKSGTASVYVCLLNFFPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 200
 Db 121 IFPPSDEQLKSGTASVYVCLLNFFPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
 QY 201 STLTLKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 238
 Db 181 STLTLKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 5
 US-09-296-005-13
 ; Sequence 13, Application US/09296005
 ; Patent No. 6290957
 ; GENERAL INFORMATION:
 ; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
 ; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
 ; FILE REFERENCE: P1123C1r
 ; CURRENT APPLICATION NUMBER: US/09/296,005
 ; CURRENT FILING DATE: 1999-04-21
 ; EARLIER APPLICATION NUMBER: US 08/887,352
 ; EARLIER FILING DATE: 1997-07-02
 ; NUMBER OF SEQ ID NOS: 26
 ; SEQ ID NO 13
 ; LENGTH: 218
 ; TYPE: PRT
 ; ORGANISM: Artificial
 ; FEATURE:
 ; NAME/KEY: Artificial

; LOCATION: 1-218
 ; OTHER INFORMATION: Light chain sequence derived from MAE11
 US-09-296-005-13

Query Match 83.4%; Score 1036; DB 4; Length 218;
 Best Local Similarity 89.9%; Pred. No. 3.1e-80;
 Matches 196; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 21 EIVLTQSPGTLSPGERATLSCASQSDYDGDSDYNNWYQOKPGQAPRLIIYAASNLES 80
 Db 1 DIQLTQSPSSLSASVGDRTITCRASQSDYDGDSDYNNWYQOKPGKAPKLLIIYAASYLE 60
 QY 81 GIPDRFSGSGGTDFLTITSLRLEPEDFAVYCCQSNEDPRTFGQGTKEIKRTVAAPSVF 140
 Db 61 GVPDRFSGSGGTDFLTITSLRLEPEDFAVYCCQSHEDPYTFGGQTKVEIKRTVAAPSVF 120
 QY 141 IFPPSDEQLKSGTASVYVCLLNFFPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 200
 Db 121 IFPPSDEQLKSGTASVYVCLLNFFPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
 QY 201 STLTLKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 238
 Db 181 STLTLKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 6
 US-09-282-505-1
 ; Sequence 1, Application US/09282505A
 ; Patent No. 6194551
 ; GENERAL INFORMATION:
 ; APPLICANT: Esche Ekinaduese Idusogie et al.
 ; TITLE OF INVENTION: Polypeptide Variants
 ; FILE REFERENCE: P1266R1
 ; CURRENT APPLICATION NUMBER: US/09/282,505A
 ; CURRENT FILING DATE: 1999-03-31
 ; NUMBER OF SEQ ID NOS: 2
 ; SEQ ID NO 1
 ; LENGTH: 218
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; NAME/KEY: Artificial Sequence
 ; LOCATION: 1-218
 ; OTHER INFORMATION: Sequence is completely synthesized
 ; Patent No. 6194551
 US-09-282-505-1

Query Match 81.6%; Score 1013; DB 4; Length 218;
 Best Local Similarity 88.1%; Pred. No. 2.7e-78;
 Matches 192; Conservative 14; Mismatches 12; Indels 0; Gaps 0;

QY 21 EIVLTQSPGTLSPGERATLSCASQSDYDGDSDYNNWYQOKPGQAPRLIIYAASNLES 80
 Db 1 DIQLTQSPSSLSASVGDRTITCRASKPVDGSDYNNWYQOKPGKAPKLLIIYAASYLE 60
 QY 81 GIPDRFSGSGGTDFLTITSLRLEPEDFAVYCCQSNEDPRTFGQGTKEIKRTVAAPSVF 140
 Db 61 GVPDRFSGSGGTDFLTITSLRLEPEDFAVYCCQSHEDPYTFGGQTKVEIKRTVAAPSVF 120
 QY 141 IFPPSDEQLKSGTASVYVCLLNFFPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 200
 Db 121 IFPPSDEQLKSGTASVYVCLLNFFPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
 QY 201 STLTLKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 238
 Db 181 STLTLKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 7
 US-09-054-255-1
 ; Sequence 1, Application US/09054255

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; Patent No. 6242195
; GENERAL INFORMATION:
; APPLICANT: Esche Ekinadese Idusogie et al.
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: P1266
; CURRENT APPLICATION NUMBER: US/09/054,255
; CURRENT FILING DATE: 1998-04-02
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: E27 anti-IgE antibody light chain
US-09-054-255-1

Query Match      81.6%; Score 1013; DB 4; Length 218;
Best Local Similarity 88.1%; Pred. No. 2.7e-78;
Matches 192; Conservative 14; Mismatches 12; Indels 0; Gaps 0;

QY 21 EIVLTSPGTLSPGERATLSCKASQSDYDGDSDYNNWYQKPGQAPRLIIYAASNLES 80
   :| | | | | :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
Db 1 DIQLTSPSSLASVSGDRVTITCRASKPVDGEGDSYNNWYQKPGKAPKLLIIYAASYLE 60
   :| | | | | :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |

QY 81 GIPDRSGSGSGTDFTLTISRLEPEDFAVYYCQSNEDPRTFGQGTKEIKRTVAAPSVF 140
   :| | | | | :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
Db 61 GVPFRSGSGSGTDFTLTISRLEPEDFAVYYCQSHEDPRTFGQGTKEIKRTVAAPSVF 120
   :| | | | | :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |

QY 141 IFPPSDEQLKSGTASVCLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDYSL 200
   :| | | | | :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
Db 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDYSL 180
   :| | | | | :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |

QY 201 STLTLSKADYKHKVACEVTHOGLSSPVTKSFNRGEC 238
   :| | | | | :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
Db 181 STLTLSKADYKHKVACEVTHOGLSSPVTKSFNRGEC 218
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RESULT 8
US-08-887-352B-15
; Sequence 15, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; FILE REFERENCE: P1266
; CURRENT APPLICATION NUMBER: US/08/887,352B
; CURRENT FILING DATE: 03-Jul-1997
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Syvoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: Amino Acids
; TOPOLOGY: Linear
US-08-887-352B-17
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```
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-15

Query Match      81.3%; Score 1010; DB 2; Length 218;
Best Local Similarity 87.6%; Pred. No. 4.8e-78;
Matches 191; Conservative 15; Mismatches 12; Indels 0; Gaps 0;

QY 21 EIVLTSPGTLSPGERATLSCKASQSDYDGDSDYNNWYQKPGQAPRLIIYAASNLES 80
   :| | | | | :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
Db 1 DIQLTSPSSLASVSGDRVTITCRASKPVDGEGDSYNNWYQKPGKAPKLLIIYAASYLE 60
   :| | | | | :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |

QY 81 GIPDRSGSGSGTDFTLTISRLEPEDFAVYYCQSNEDPRTFGQGTKEIKRTVAAPSVF 140
   :| | | | | :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
Db 61 GVPFRSGSGSGTDFTLTISRLEPEDFAVYYCQSHEDPRTFGQGTKEIKRTVAAPSVF 120
   :| | | | | :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |

QY 141 IFPPSDEQLKSGTASVCLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDYSL 200
   :| | | | | :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
Db 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDYSL 180
   :| | | | | :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |

QY 201 STLTLSKADYKHKVACEVTHOGLSSPVTKSFNRGEC 238
   :| | | | | :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
Db 181 STLTLSKADYKHKVACEVTHOGLSSPVTKSFNRGEC 218
   :| | | | | :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |

RESULT 9
US-08-887-352B-17
; Sequence 17, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; FILE REFERENCE: P1266
; CURRENT APPLICATION NUMBER: US/08/887,352B
; CURRENT FILING DATE: 03-Jul-1997
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Syvoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-17

Query Match      81.3%; Score 1010; DB 2; Length 218;
Best Local Similarity 87.6%; Pred. No. 4.8e-78;
Matches 191; Conservative 15; Mismatches 12; Indels 0; Gaps 0;

QY 21 EIVLTSPGTLSPGERATLSCKASQSDYDGDSDYNNWYQKPGQAPRLIIYAASNLES 80
   :| | | | | :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
Db 1 DIQLTSPSSLASVSGDRVTITCRASKPVDGEGDSYNNWYQKPGKAPKLLIIYAASYLE 60
   :| | | | | :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
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QY 81 GIPDRFSGSGGTDTFTLTISRLEPEDFAVYYCQOSNEDPRTFGQGTKEIKRTVAAPSVF 140
Db 61 GVPSRFSGSGGTDTFTLTISRLEPEDFAVYYCQOSHEDPYTFGGTKVEIKRTVAAPSVF 120
QY 141 IFPPSDEQLKGTASVWCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 200
Db 121 IFPPSDEQLKGTASVWCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 180
QY 201 STLTLSKADYEKKHKYACEVTHQGLSSPVTKSFNRGEC 238
Db 181 STLTLSKADYEKKHKYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 10
US-08-887-352B-19
; Sequence 19, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-19

Query Match 81.3%; Score 1010; DB 2; Length 218;
Best Local Similarity 87.6%; Pred. No. 4.8e-78;
Matches 191; Conservative 15; Mismatches 12; Indels 0; Gaps 0;

QY 21 EIVLTQSPGTLISLSPGERATLSCAKASQVDYDGSYMNWYQOKPGQAPRLLIYAASNLES 80
Db 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQOKPGKAPKLLIYAASYLE 60
QY 81 GIPDRFSGSGGTDTFTLTISRLEPEDFAVYYCQOSNEDPRTFGQGTKEIKRTVAAPSVF 140
Db 61 GVPSRFSGSGGTDTFTLTISRLEPEDFAVYYCQOSHEDPYTFGGTKVEIKRTVAAPSVF 120
QY 141 IFPPSDEQLKGTASVWCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 200
Db 121 IFPPSDEQLKGTASVWCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 180
QY 201 STLTLSKADYEKKHKYACEVTHQGLSSPVTKSFNRGEC 238
Db 181 STLTLSKADYEKKHKYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 12
US-09-109-207C-15
; Sequence 15, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypept
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
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RESULT 11
US-08-887-352B-24
; Sequence 24, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-24

Query Match 81.3%; Score 1010; DB 2; Length 218;
Best Local Similarity 87.6%; Pred. No. 4.8e-78;
Matches 191; Conservative 15; Mismatches 12; Indels 0; Gaps 0;

QY 21 EIVLTQSPGTLISLSPGERATLSCAKASQVDYDGSYMNWYQOKPGQAPRLLIYAASNLES 80
Db 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQOKPGKAPKLLIYAASYLE 60
QY 81 GIPDRFSGSGGTDTFTLTISRLEPEDFAVYYCQOSNEDPRTFGQGTKEIKRTVAAPSVF 140
Db 61 GVPSRFSGSGGTDTFTLTISRLEPEDFAVYYCQOSHEDPYTFGGTKVEIKRTVAAPSVF 120
QY 141 IFPPSDEQLKGTASVWCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 200
Db 121 IFPPSDEQLKGTASVWCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 180
QY 201 STLTLSKADYEKKHKYACEVTHQGLSSPVTKSFNRGEC 238
Db 181 STLTLSKADYEKKHKYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 12
US-09-109-207C-15
; Sequence 15, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypept
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
```


US-09-109-207C-24

Query Match		81.3%;	Score 1010;	DB 4;	Length 218;
Best Local Similarity		87.6%;	Pred. No. 4.8e-78;		
Matches 191;		Conservative 15;	Mismatches 12;	Indels 0;	Gaps 0;
Qy	21	EIVLTQSPGTLSPGERATLSCRASQSVYDGDSDYNNWYQOKPGQAPRLLIYAASNLES	80		
Db	1	DIQLTQSPFSSLSASVGDRTTICRASKFVDGEGSYLNWYQOKPGKAPKLLIYAASYLE	60		
Qy	81	GIPDRFSGSGGTDFLTISRLPEDPFVYVYCCQSNEDPRTFGGCTKLEIKRTVAAPSVF	140		
Db	61	GVPFRFSGSGGTDFLTISRLQPEDFATYVYCCQSHEDPYTFGGCTKVEIKRTVAAPSVF	120		
Qy	141	IFPPSDEQLKSGTASVVCCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSTYSLS	200		
Db	121	IFPPSDEQLKSGTASVVCCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSTYSLS	180		
Qy	201	STLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	238		
Db	181	STLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	218		

Search completed: April 17, 2002, 16:39:21
Job time: 144 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 17, 2002, 16:37:07 ; Search time 25.85 Seconds
(without alignments)
701.336 Million cell updates/sec

Title: US-09-499-662-107
Perfect score: 1242
Sequence: 1 METDITLLWVLLWVPGSNG.....EVTHQGLSSPVTKSFNRGEC 238

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	996.5	80.2	215	2 JE0242	Ig kappa chain NIG
2	950.5	76.5	215	2 JE0244	Ig kappa chain NIG
3	941.5	75.8	215	2 A23746	Ig kappa chain V-I
4	927.5	74.7	215	2 JE0243	Ig kappa chain NIG
5	884	71.2	216	2 JE0241	Ig kappa chain Am3
6	801	64.5	240	2 S06084	Ig kappa chain pre
7	749	60.3	218	2 S68241	Ig kappa chain V r
8	743	59.8	218	2 JC5810	monoclonal antibody
9	723	58.2	220	2 A31790	Ig kappa chain V r
10	722	58.1	234	2 S14237	Ig kappa chain pre
11	720.5	58.0	219	2 PC4203	Ig kappa chain (mo
12	720.5	58.0	219	2 S38865	Ig kappa chain - m
13	714.5	57.5	219	2 S52028	Ig kappa chain - m
14	714	57.5	210	2 A56169	Ig kappa chain V r
15	712.5	57.4	225	2 S37484	Ig kappa chain - m
16	711.5	57.3	230	2 S33161	Ig kappa chain - s
17	708.5	57.0	217	2 S42772	Ig kappa chain - m
18	699.5	56.3	235	2 S25058	Ig kappa chain - m
19	698.5	56.2	219	2 S16112	Ig kappa chain V r
20	692	55.7	234	2 S01320	Ig kappa chain pre
21	690.5	55.6	225	2 JL0029	Ig kappa chain pre
22	687	55.3	214	2 S68212	Ig kappa chain (Ma
23	622	50.1	178	2 PT0219	Ig kappa chain V-C
24	614.5	49.5	197	2 S29593	Ig kappa chain (WM
25	605.5	48.8	135	2 S52059	JC-kappa protein -
26	583	46.9	144	2 PL0106	Ig kappa chain pre
27	582.5	46.9	229	2 A20969	Ig kappa chain pre
28	576	46.4	131	2 PH1226	Ig kappa chain pre
29	564.5	45.5	145	2 S20631	Ig kappa chain - n

30	563.5	45.4	238	2 A49633	Ig lambda-like cha
31	548	44.1	106	1 K3HU	Ig kappa chain C r
32	541.5	43.6	129	1 K3HUHA	Ig kappa chain pre
33	539.5	43.4	128	2 S20636	Ig kappa chain V r
34	536.5	43.2	129	2 S49532	anti-5m antibody V
35	528.5	42.6	129	1 K3HUHI	Ig kappa chain pre
36	528	42.5	131	1 KVM5M6	Ig kappa chain pre
37	525.5	42.3	129	2 S46369	Ig light chain var
38	525.5	42.3	134	2 S38643	Ig kappa chain V r
39	516.5	41.6	129	2 A32274	Ig kappa chain pre
40	513	41.3	99	2 A37927	Ig kappa chain C r
41	511	41.1	128	2 A56701	Ig kappa chain V r
42	510	41.1	132	1 KVM532	Ig kappa chain pre
43	508	40.9	233	2 S29577	Ig light chain - r
44	507	40.8	99	2 S26653	Ig kappa chain C r
45	505.5	40.7	130	2 S20637	Ig kappa chain V r

ALIGNMENTS

RESULT 1
JE0242
Ig kappa chain NIG26 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0242
R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda
submitted to JIPID, November 1998
A:Description: Structure relationship of kappa type light chains with AL amyloidosis:
A:Reference number: JE0241
A:Accession: JE0242
A:Molecule type: protein
A:Residues: 1-215 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 80.2%; Score 996.5; DB 2; Length 215;
Best Local Similarity 89.4%; Pred. No. 1.7e-57;
Matches 195; Conservative 8; Mismatches 12; Indels 3; Gaps 1;

Qy	21	EIVLTQSPGTLSPGERATLSCAKASQSDVDGDSVMYQKPGQAPRLIIYAASNLES	80
Db	1	EIVLTQSPGTLSPGERATLSCASQSV---SNNYLAWYQKPGQAPSLIIYDASSRAT	57
Qy	81	GIPDRFSGSGGTFTLISRLEPEDFAVYYCQQSNEDPRTFGQGTCKLEIKRTVAAPSVF	140
Db	58	GIPDRFSGSGGTFTLISRLEPEDFAVYYCQQYDRPPTFGQGTCKLEIKRTVAAPSVF	117
Qy	141	IFPPSDEQLKSGTASVWCCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLS	200
Db	118	IFPPSDEQLKSGTASVWCCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLS	177
Qy	201	STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC	238
Db	178	STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC	215

RESULT 2
JE0244
Ig kappa chain NIG2 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0244
R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.
submitted to JIPID, November 1998
A:Description: A new subgroup of k type light chains (VkV) identified in cases of AL
A:Reference number: JE0243
A:Accession: JE0244
A:Molecule type: protein
A:Residues: 1-215 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology

R:Crowe, J.S.; Smith, M.A.; Cooper, H.J.

Nucleic Acids Res. 17, 1989

A:Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNA

A:Reference number: S06084; MUID:9001688

A:Accession: S06084

A:Molecule type: mRNA

A:Residues: 1-240 <CRO>

A:Cross-references: EMBL:X16129; NID:956457; PIDN:CAA34256.1; PID:956458

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-240/Product: Ig kappa chain #status predicted <MAT>

F:153-222/Domain: immunoglobulin homology <IMM>

Query Match 64.5%; Score 801; DB 2; Length 240;
Best Local Similarity 62.5%; Pred. No. 6.8e-45;
Matches 150; Conservative 37; Mismatches 51; Indels 2; Gaps 1;

QY 1 METDTILLVLLWVPGTGEIVLTQSPGTLSPGERATLSCSKASQSDYDGD--SYMN 58

Db 1 MESQTQVLSLLWISGTGDFVMTQSPSSLAIVSAGETVLTINCKSSQSLFYSGNKNYLA 60

QY 59 WYQKPGQAPRLIYAASNLGSPDRFSGSGCTFTLTISRLEPEFAVYVCOQSNED 118

Db 61 WYQKPGQSKLLIYWASTRQSGVDPDRFISGSGCTFTLTISVQAEALAIYVCLQYET 120

QY 119 PRTEGQGTLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNAL 178

Db 121 PYTFGAGTKLELRADAAPTIFPPSTEQALATGASVVCCLNNFYPDRISVKKIDGTE 180

QY 179 QSGNSQSVTEQDSKDSYSLSSLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 238

Db 181 RROGVLDVTDQDSKDSYSLSSLTLSKADYEHSHNLTCEVHKTSPPVVKSFNRNEC 240

RESULT 7

S68241

Ig kappa chain V region (Mab13-1) - mouse (fragment)

N:Alternate names: immunoglobulin light chain

C:Species: Mus musculus (house mouse)

C:Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000

C:Accession: S68241; S68214

R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Imanaka, T.

submitted to the EMBL Data Library, March 1994

A:Description: Specific peroxidase activity by formation of an antibody L-chain-porphyrin

A:Reference number: S68241

A:Accession: S68241

A:Molecule type: mRNA

A:Residues: 1-218 <TAK>

A:Cross-references: EMBL:D29670; NID:9473962; PIDN:BA06141.1; PID:9473963

R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Imanaka, T.

FEBS Lett. 375, 273-276, 1995

A:Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin

A:Reference number: S68211; MUID:96085223

A:Accession: S68214

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 'N1', 3-212 <TAW>

A:Cross-references: EMBL:D29670

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

Query Match 60.3%; Score 749; DB 2; Length 218;
Best Local Similarity 64.7%; Pred. No. 1.4e-41;
Matches 141; Conservative 29; Mismatches 48; Indels 0; Gaps 0;

QY 21 EIVLTQSPGTLSPGERATLSCSKASQSDYDGSYNWYQKPGQAPRLIYAASNLDS 80

Db 1 ELVLTQSPASLAVSLGQRATISCRASKSVASGYIYHMYQKPGQPKLLISLATNLES 60

QY 81 GIPDRFSGSGSGTFTLTISRLEPEFAVYVCOQSNEDPRTEFGQGTLEIKRTVAAPSVF 140

Db 61 GVPARFSGSGSGTFTLTINHPVEEDVATYVCOHSRELPLTFGAGTKLELRADAAPTIVS 120

QY 141 IFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQSVTEQDSKDSYSLDS 200

Db 121 IFPPSSEQLTSGGASVVCFLNNFYPKIDNVKWKIDGSRQNCVLSWTDQDSKDSYSLDS 180

QY 201 STLTLKADYKHKHYACEVTHQGLSSPVTKSFNRGEC 238

Db 181 STLTLTKDEYERHNSYTCETHTKTSTSPVKSFNRGEC 218

RESULT 8

JC5810

monoclonal antibody 13-1 light chain - mouse

C:Species: Mus musculus (house mouse)

C:Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000

C:Accession: JC5810

R:Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada,

Biochem. Biophys. Res. Commun. 240, 566-572, 1997

A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porp

A:Reference number: JC5810; MUID:98063277

A:Accession: JC5810

A:Molecule type: protein

A:Residues: 1-218 <AKA>

C:Comment: This catalytic antibody has peroxidase oxidase. It is directed against a p

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 59.8%; Score 743; DB 2; Length 218;

Best Local Similarity 65.0%; Pred. No. 3.3e-41;

Matches 141; Conservative 27; Mismatches 49; Indels 0; Gaps 0;

QY 22 IVLTQSPGTLSPGERATLSCSKASQSDYDGSYNWYQKPGQAPRLIYAASNLDSG 81

Db 2 IVLTQSPASLAVSLGQRATISCRASKSVASGYIYHMYQKPGQPKLLISLASNLDSG 61

QY 82 IPDRFSGSGSGTFTLTISRLEPEFAVYVCOQSNEDPRTEFGQGTLEIKRTVAAPSVFI 141

Db 62 VPARFSGSGSGTFTLTINHPVEEDVATYVCOHSRELPLTFGAGTKLELRADAAPTIVSI 121

QY 142 FPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQSVTEQDSKDSYSLSS 201

Db 122 FPPSSEQLTSGGASVVCFLNNFYPKIDNVKWKIDGSRQNCVLSWTDQDSKDSYSLSS 181

QY 202 TLTLKADYKHKHYACEVTHQGLSSPVTKSFNRGEC 238

Db 182 TLTLTKDEYERHNSYTCETHTKTSTSPVKSFNRNEC 218

RESULT 9

A31790

Ig kappa chain V region (17/9) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000

C:Accession: A31790

R:Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A

J. Biol. Chem. 263, 17100-17105, 1988

A:Title: Preliminary crystallographic data, primary sequence, and binding data for an

A:Reference number: A92686; MUID:89034213

A:Accession: A31790

A:Molecule type: mRNA

A:Residues: 1-220 <SCH>

A:Cross-references: GB:M23626; GB:J04061; NID:9533234; PIDN:AAA39162.1; PID:9533235

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 58.2%; Score 723; DB 2; Length 220;

Best Local Similarity 60.9%; Pred. No. 6.5e-40;

Matches 134; Conservative 35; Mismatches 49; Indels 2; Gaps 1;


```

RESULT 15
S37484
Ig kappa chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000
C:Accession: S37484
R:Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A:reference number: S37483
A:Accession: S37484
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-225 <DUC>
A:Cross-references: EMBL:X70424; NID:g406254; PIDN:CARA49869.1; PID:g406255
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin

```

[illegible]

QY 191 DSKDSTYSILSTLTISKADYEKHKYACEVTHQGLSSPVTXSFNRGEC 238
 |||||:|||||: ||: | || | : ||: ||||| ||
 Db 178 DSKDSTYSMSSILTTKDEYEHNSYTCETHTKTSTSPVKSFNREC 225

Search completed: April 17, 2002, 16:39:53
Job time: 166 sec

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OM protein - protein search, using sw model

Run on: April 17, 2002, 16:38:12 ; Search time 17.09 Seconds
(without alignments)
510.604 Million cell updates/sec

Title: US-09-499-662-107

Perfect score: 1242

Sequence: 1 METDILLWVLLWVPGSTG.....EVTHQGLSPVTKSFNRGEC 238

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	548	44.1	106	1 KAC_HUMAN	P01834 homo sapien
2	541.5	43.6	129	1 KV3L_HUMAN	P18135 homo sapien
3	538.5	42.6	129	1 KV3M_HUMAN	P18136 homo sapien
4	528	42.5	131	1 KV3I_MOUSE	P01661 mus sapien
5	510	41.1	132	1 KV3F_MOUSE	P01658 mus sapien
6	494	39.8	128	1 KV3K_HUMAN	P06311 homo sapien
7	478	38.5	111	1 KV3M_MOUSE	P01665 mus sapien
8	476	38.3	111	1 KV3N_MOUSE	P01666 mus sapien
9	474	38.2	111	1 KV3O_MOUSE	P01667 mus sapien
10	471	37.9	111	1 KV3Q_MOUSE	P01669 mus sapien
11	469.5	37.8	109	1 KV3B_HUMAN	P01620 homo sapien
12	468.5	37.7	109	1 KV3D_HUMAN	P01622 homo sapien
13	468.5	37.7	129	1 KV3H_HUMAN	P04207 homo sapien
14	464.5	37.4	109	1 KV3E_HUMAN	P01623 homo sapien
15	463	37.3	111	1 KV3L_MOUSE	P01664 mus sapien
16	455	36.6	115	1 KV3I_HUMAN	P04433 homo sapien
17	453.5	36.5	110	1 KV3P_MOUSE	P01668 mus sapien
18	447.5	36.0	109	1 KV3G_HUMAN	P04206 homo sapien
19	442	35.6	134	1 KV4C_HUMAN	P06314 homo sapien
20	436.5	35.1	108	1 KV3A_HUMAN	P01619 homo sapien
21	433.5	34.9	133	1 KV2F_HUMAN	P06310 homo sapien
22	431	34.7	111	1 KV3H_MOUSE	P01660 mus sapien
23	429.5	34.6	116	1 KV3J_HUMAN	P04434 homo sapien
24	426.5	34.3	133	1 KV4B_HUMAN	P06313 homo sapien
25	423	34.1	111	1 KV3J_MOUSE	P01662 mus sapien
26	422	34.0	111	1 KV3K_MOUSE	P01663 mus sapien
27	422	34.0	129	1 KV1W_HUMAN	P04431 homo sapien
28	415	33.4	111	1 KV3R_MOUSE	P01670 mus sapien
29	411.5	33.1	109	1 KV3F_HUMAN	P01624 homo sapien
30	409.5	33.0	100	1 KV3C_HUMAN	P01621 homo sapien
31	408	32.9	114	1 KV4A_HUMAN	P01625 homo sapien
32	407	32.8	111	1 KV3S_MOUSE	P01671 mus sapien
33	406	32.7	111	1 KV3U_MOUSE	P01673 mus sapien

ALIGNMENTS

RESULT 1

KAC_HUMAN	STANDARD;	PRT;	106 AA.
ID	KAC_HUMAN		
AC	P01834;		
DT	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)		
DT	20-AUG-2001 (Rel. 40, Last annotation update)		
DE	IG KAPPA CHAIN C REGION.		
GN	IGKC.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE (MYELOMA PROTEIN EU).		
RX	MEDLINE=71064023; PubMed=5489770;		
RA	Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;		
RT	"The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain.";		
RT	Biochemistry 9:3155-3161(1970).		
RL	[2]		
RP	DISULFIDE BONDS.		
RX	MEDLINE=71064027; PubMed=4923144;		
RA	Gall W.E., Edelman G.M.;		
RT	"The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds.";		
RL	Biochemistry 9:3188-3196(1970).		
RN	[3]		
RP	SEQUENCE (BENCE-JONES PROTEIN TI).		
RX	MEDLINE=72188439; PubMed=5027703;		
RA	Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;		
RT	"Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein TI). IV. The complete amino acid sequence and its significance for the mechanism of antibody production.";		
RT	Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).		
RN	[4]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=8104304; PubMed=6775818;		
RA	Hietter P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.;		
RT	"Cloned human and mouse kappa immunoglobulin constant and J region genes conserve homology in functional segments.";		
RL	Cell 22:197-207(1980).		
RN	[5]		
RP	SEQUENCE (BENCE-JONES PROTEIN ROY).		
RA	Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H., Steinmetz-Kayne M., Suter L., Watanabe S.;		
RL	(In) Franek F., Shugar D. (eds.);		
RL	Gamma globulins: structure and function, pp.57-74, Academic Press, New York (1969).		
RN	[6]		
RP	SEQUENCE (BENCE-JONES PROTEIN CUM).		
RX	MEDLINE=68242259; PubMed=5586923;		
RA	Hilschmann N.;		
RT	"The complete amino acid sequence of Bence Jones protein Cum (kappa-type).";		

P01659 mus musculus
P01603 homo sapien
P01672 mus musculus
P01600 homo sapien
P01656 mus musculus
P01654 mus musculus
P01605 homo sapien
P01606 homo sapien
P06309 homo sapien
P01599 homo sapien
P01617 homo sapien
P01655 mus musculus

34 404 32.5 112 1 KV3G_MOUSE
35 401 32.3 108 1 KV3T_HUMAN
36 401 32.3 111 1 KV3T_MOUSE
37 400 32.2 108 1 KV1H_HUMAN
38 400 32.2 111 1 KV3C_MOUSE
39 397 32.0 111 1 KV3A_MOUSE
40 395 31.8 108 1 KV1M_HUMAN
41 394 31.7 108 1 KV2E_HUMAN
42 393.5 31.7 117 1 KV1G_HUMAN
43 391 31.5 108 1 KV2D_HUMAN
44 390.5 31.4 113 1 KV3B_MOUSE
45 389.5 31.4 112 1 KV3B_MOUSE

RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
 RN [7]
 RP SEQUENCE (BENCE-JONES PROTEIN AG).
 RX MEDLINE=69234734; PubMed=4893682;
 RA Titani K., Shinoda T., Putnam F.W.;
 RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
 RT complete sequence and the location of the disulfide bridges.";
 RL J. Biol. Chem. 244:3350-3360(1969).
 RN [8]
 RP SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
 RX MEDLINE=70201507; PubMed=5447531;
 RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
 RT "Macroglobulin structure: variable sequence of light and heavy
 RT chains.";
 RL Science 169:56-59(1970).
 CC -!- MISCELLANEOUS: THE EU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER,
 CC 45-ALA & 83-VAL. THE ROY SEQUENCE HAS THE INV (1,2) ALLOTYPIC
 CC MARKER, 45-ALA AND 83-LEU.
 CC -----
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 CC -----
 DR EMBL; J00241; AAA58989.1; -;
 DR EMBL; V00557; CAA23823.1; -;
 DR PIR; A02116; K3HU.
 DR MIM; 147200;
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003597; Ig_c1.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00407; IgC1; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1 1
 FT DISULFID 26 86
 FT DISULFID 106 106
 FT VARIANT 83 83
 FT INTERCHAIN (WITH A HEAVY CHAIN).
 FT V -> L (IN INV(1,2) MARKER).
 FT /FTIG-VAR_003897.
 FT D -> N (IN REF. 7 AND 8).
 FT E -> Q (IN REF. 5 AND 6).
 FT CONFLICT 14 14
 FT CONFLICT 57 57
 FT SEQUENCE 106 AA; 11609 MW; 5198401FDD372CE8 CRC64;
 SQ
 Query Match 44.1%; Score 548; DB 1; Length 106;
 Best Local Similarity 100.0%; Pred. No. 1.6e-38; Mismatches 0; Indels 0; Gaps 0;
 Matches 106; Conservative 0;
 QY 133 TVAAPSVFIFPPSDEQLKSGTASVVCCLNFFPREAKVQWKVDNALQSGNSQESVTEQDS 192
 Db 1 TVAAPSVFIFPPSDEQLKSGTASVVCCLNFFPREAKVQWKVDNALQSGNSQESVTEQDS 60
 QY 193 KSTYSLSTLTLKADYKHKYKVIACEVTHQGLSSPVTKSFNRGEC 238
 Db 61 KDSTYSLSTLTLKADYKHKYKVIACEVTHQGLSSPVTKSFNRGEC 106
 RESULT 2
 ID KV3L_HUMAN STANDARD; PRT; 129 AA.
 AC P18135;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION HAH PRECURSOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=88171307; PubMed=3127527;
 RA Kippes T.J., Tomhave E., Chen P.P., Carson D.A.;
 RT "Autoantibody-associated kappa light chain variable region gene
 RT expressed in chronic lymphocytic leukemia with little or no somatic
 RT mutation. Implications for etiology and immunotherapy.";
 RL J. Exp. Med. 167:840-852(1988).
 CC -!- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
 CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
 CC LEUKEMIA.
 CC PIR; PLO022; K3HUHA.
 DR HSSP; P01789; 2MCP.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IgV; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HAH.
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 56 70 FRAMEWORK 2.
 FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 78 109 FRAMEWORK 3.
 FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 119 129 JK1 SEGMENT.
 FT DISULFID 43 109 BY SIMILARITY.
 FT NON_TER 129 129
 FT SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64;
 SQ
 Query Match 43.6%; Score 541.5; DB 1; Length 129;
 Best Local Similarity 80.3%; Pred. No. 6.9e-38;
 Matches 106; Conservative 9; Mismatches 14; Indels 3; Gaps 1;
 QY 1 METDITLLWVLLWVPGSTGEIVLTQSPGTLSLSPGERATLSCAKSQSVVDYDGSYNNWY 60
 Db 1 METPAQLLFLLWLEDDTTEGIVLTQSPGTLSLSPGERATLSCRSQSV---SSYLAWY 57
 QY 61 QKQPGAPRLIIYAASNLSESGIDPDRFSGSGSDFTLTISRLEPEDFANYVCOOSNEDPR 120
 Db 58 QKQPGAPRLIIYGASSRATGIPDRFSGSGSDFTLTISRLEPEDFANYVCOQYGTSPR 117
 QY 121 TFGQGTKEIKR 132
 Db 118 TFGQGTKEIKR 129
 RESULT 3
 ID KV3M_HUMAN STANDARD; PRT; 129 AA.
 AC P18136;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION HIC PRECURSOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88171307; PubMed=3127527;
 RA Kippes T.J., Tomhave E., Chen P.P., Carson D.A.;
 RT "Autoantibody-associated kappa light chain variable region gene
 RT expressed in chronic lymphocytic leukemia with little or no somatic
 RT mutation. Implications for etiology and immunotherapy.";
 RL J. Exp. Med. 167:840-852(1988).
 CC -!- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
 CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
 CC LEUKEMIA.
 CC PIR; PLO021; K3HUHI.
 DR HSSP; P01789; 2MCP.
 DR

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DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HIC.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 56 70 FRAMEWORK 2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 78 109 FRAMEWORK 3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14070 MW; 7395528EA2BB74D6 CRC64;

Query Match 42.6%; Score 528.5; DB 1; Length 129;
Best Local Similarity 78.8%; Pred. No. 8.1e-37;
Matches 104; Conservative 9; Mismatches 16; Indels 3; Gaps 1;

QY 1 METDTILLWLLVLPSTGEIVLTQSPGTLISLSPGERATLSCRAQSQSYVDYDSDSYMNY 60
   ||| ||:||||:| :|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:
DB 1 METPAQLLFLLLLWLPDTTGEIVLTQSPGTLISLSPGERATLSCRAQSQSYV---SSYLAWY 57
   ||| ||:||||:| :|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:

QY 61 QOKPQAPRLIYAASNLSEGIPIRFGSGSGTDTFTLTISRLEPEDFAVYVYQQSNEDPR 120
   |||||:|||||||:|:|||||||:|||||||:|||||||:|||||||:|:|||||||:
DB 58 QOKPQAPRLIYGASSRATGIPDRFGSGSGTDTFTLTISRLEPDXFAVYVYQQYGSPPW 117
   |||||:|||||||:|:|||||||:|||||||:|||||||:|||||||:|:|||||||:

QY 121 TFGQGTKEIKR 132
   |||||:|||||||:
DB 118 TFGQGTKEIKR 129
   |||||:|||||||:

RESULT 4
KV3F_MOUSE STANDARD; PRT; 131 AA.
AC P01661;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION MOPC 63 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 1-35.
RX MEDLINE=78235887; PubMed=98179;
RA Burstein Y., Schechter I.;
RT "Primary structures of N-terminal extra peptide segments linked to
RT the variable and constant regions of immunoglobulin light chain
RT precursors: implications on the organization and controlled
RT expression of immunoglobulin genes.";
RL Biochemistry 17:2392-2400(1978).
RN [2]
RP SEQUENCE OF 21-131.
RX MEDLINE=73140225; PubMed=4691517;
RA McKean D.J., Potter M., Hood L.E.;
RT "Mouse immunoglobulin chains. Pattern of sequence variation among
RT kappa chains with limited sequence differences.";
RL Biochemistry 12:760-771(1973).
RN [3]
RP REVISTONS
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
DR PIR; A01935; KVM5M6.
DR InterPro; IPR003006; Ig_MHC.

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DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 131 IG KAPPA CHAIN V-III REGION MOPC 63.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 59 73 FRAMEWORK 2.
FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 81 112 FRAMEWORK 3.
FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 122 131 FRAMEWORK 4.
FT DISULFID 43 112 BY SIMILARITY.
FT NON_TER 131 131
SQ SEQUENCE 131 AA; 14291 MW; D212EC9F08DC880A CRC64;

Query Match 42.5%; Score 528; DB 1; Length 131;
Best Local Similarity 75.6%; Pred. No. 9.1e-37;
Matches 99; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

QY 1 METDTILLWLLVLPSTGEIVLTQSPGTLISLSPGERATLSCRAQSQSYVDYDSDSYMNY 60
   |||||:|||||||:|:|||||||:|||||||:|||||||:|||||||:|:|||||||:
DB 1 METDTILLWLLVLPSTGEIVLTQSPASLAVSLGORATISCRASESDYSYNSFHWY 60
   |||||:|||||||:|:|||||||:|||||||:|||||||:|||||||:|:|||||||:

QY 61 QOKPQAPRLIYAASNLSEGIPIRFGSGSGTDTFTLTISRLEPEDFAVYVYQQSNEDPR 120
   |||||:|||||||:|:|||||||:|||||||:|||||||:|||||||:|:|||||||:
DB 61 QOKPQAPRLIYLAASNLSEGIPIRFGSGSGTDTFTLTIDPVEADDAATYVYQQNNEDPW 120
   |||||:|||||||:|:|||||||:|||||||:|||||||:|||||||:|:|||||||:

QY 121 TFGQGTKEIKR 131
   ||| |||||:
DB 121 TFGQGTKEIKR 131
   ||| |||||:

RESULT 5
KV3F_MOUSE STANDARD; PRT; 132 AA.
AC P01658;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION MOPC 321 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 1-37.
RX MEDLINE=78235887; PubMed=98179;
RA Burstein Y., Schechter I.;
RT "Primary structures of N-terminal extra peptide segments linked to
RT the variable and constant regions of immunoglobulin light chain
RT precursors: implications on the organization and controlled
RT expression of immunoglobulin genes.";
RL Biochemistry 17:2392-2400(1978).
RN [2]
RP SEQUENCE OF 21-132.
RX MEDLINE=73140224; PubMed=4120629;
RA McKean D.J., Potter M., Hood L.E.;
RT "Mouse immunoglobulin chains. Partial amino acid sequence of a kappa
RT chain.";
RL Biochemistry 12:749-759(1973).
CC -1- MISCELLANEOUS: THE PARTIAL SEQUENCE OF THE C REGION OF THIS
CC BENCE-JONES PROTEIN WAS ALSO DETERMINED. IT DIFFERS FROM THAT
CC REPORTED FOR MOUSE MOPC 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY
CC RESIDUES.
DR PIR; A01933; KVM532.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein; Signal.

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RESULT 8
KV3N_MOUSE
ID KV3N_MOUSE STANDARD; PRT; 111 AA.
AC P01667;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 7183.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR PIR; B01937; KVM583.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11952 MW; 2058BB50CE306D31 CRC64;

Query Match 38.38; Score 476; DB 1; Length 111;
Best Local Similarity 81.1%; Pred. No. 1.3e-32;
Matches 90; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Qy 21 EIVLTQSPGTLSPGERATLSCASQSDVDGDSYNNWYQKPGQAPRLLIYAASNLES 80
Db 1 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYNNWYQKPGQAPRLLIYAASNLES 60
Qy 81 GIPDRFGSGSGTDFTLNISRLPEDEFAVYVYCOQSNEDPRTFGQGTKLEIK 131
Db 61 GIPARFSGSGSGTDFTLNIHPVEEDAATYYCQSQNEDPLTFGAGTKLEIK 111

RESULT 9
KV3O_MOUSE
ID KV3O_MOUSE STANDARD; PRT; 111 AA.
AC P01667;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 6308.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR PIR; C01937; KVM508.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.

Query Match 37.9%; Score 471; DB 1; Length 111;
Best Local Similarity 80.2%; Pred. No. 3.5e-32;
Matches 89; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

Qy 21 EIVLTQSPGTLSPGERATLSCASQSDVDGDSYNNWYQKPGQAPRLLIYAASNLES 80
Db 1 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYNNWYQKPGQAPRLLIYAASNLES 60
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DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12071 MW; 7A4ADE4D6C256D29 CRC64;

Query Match 38.2%; Score 474; DB 1; Length 111;
Best Local Similarity 81.1%; Pred. No. 2e-32;
Matches 90; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

Qy 21 EIVLTQSPGTLSPGERATLSCASQSDVDGDSYNNWYQKPGQAPRLLIYAASNLES 80
Db 1 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYNNWYQKPGQAPRLLIYAASNLES 60
Qy 81 GIPDRFGSGSGTDFTLNISRLPEDEFAVYVYCOQSNEDPRTFGQGTKLEIK 131
Db 61 GIPARFSGSGSGTDFTLNIHPVEEDAATYYCQSQNEDPRTFGSGTKLEIK 111

RESULT 10
KV3Q_MOUSE
ID KV3Q_MOUSE STANDARD; PRT; 111 AA.
AC P01669;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION PC 7769.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR PIR; E01937; KVM569.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12011 MW; 6FAA345279356829 CRC64;

Query Match 37.9%; Score 471; DB 1; Length 111;
Best Local Similarity 80.2%; Pred. No. 3.5e-32;
Matches 89; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

Qy 21 EIVLTQSPGTLSPGERATLSCASQSDVDGDSYNNWYQKPGQAPRLLIYAASNLES 80
Db 1 DIVLTQSPASLAVSLGQRATISCKASQSDVDGDSYNNWYQKPGQAPRLLIYAASNLES 60
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QY 81 GIPDRFSGSGTDTLTISRLEPDAFYVYCOQSNEDPRTFGGQTKLEIK 131
||| ||||||||||||| : ||| ||||||||||||| ||| |||||||
Db 61 GIPARFSGSGTDTLTNIHPVEEDAATYVYCOQSNEDPRTFGGQTKLEIK 111

RESULT 11

KV3B_HUMAN STANDARD; PRT; 109 AA.
ID KV3B_HUMAN
AC P01620;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION SIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human Igm anti-gamma-globulins of the Wa
RT group."
RL Biochemistry 20:5816-5822(1981).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR; A01892; K3HUSI.
DR HSP; P01789; 2MCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
KW DISULFID 23 89
FT NON_TER 109 109
FT BY SIMILARITY.
SQ SEQUENCE 109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;

Query Match 37.8%; Score 469.5; DB 1; Length 109;
Best Local Similarity 81.2%; Pred. No. 4.5e-32;
Matches 91; Conservative 9; Mismatches 9; Indels 3; Gaps 1;

QY 21 EIVLTQSPGTLSPGERATLSCASQSVYDGSYMNWYQKPGQAPRLIYAASNLES 80
||||| ||||||||||||| : ||| ||||||||||||| ||| |||||||
Db 1 EIVLTQSPGTLSPGERATLSCASQSVYDGSYMNWYQKPGQAPRLIYAASNLES 57

QY 81 GIPDRFSGSGTDTLTISRLEPDAFYVYCOQSNEDPRTFGGQTKLEIK 132
||||| ||||||||||||| : ||| ||||||||||||| ||| |||||||
Db 58 GIPDRFSGSGTDTLTISRLEPDAFYVYCOQSGSPDTFGGQSKVEIKR 109

RESULT 12

KV3D_HUMAN STANDARD; PRT; 109 AA.
ID KV3D_HUMAN
AC P01622;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION TI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72188439; PubMed=5027703;
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
RT ti). IV. The complete amino acid sequence and its significance for
RT the mechanism of antibody production."
RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).

CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
CC PIR; A01895; K3HUTI.
DR HSP; P01789; 2MCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
KW DISULFID 23 89
FT NON_TER 109 109
FT BY SIMILARITY.
SQ SEQUENCE 109 AA; 11788 MW; 8C35058CDC7749BC CRC64;

Query Match 37.7%; Score 468.5; DB 1; Length 109;
Best Local Similarity 81.2%; Pred. No. 5.4e-32;
Matches 91; Conservative 8; Mismatches 10; Indels 3; Gaps 1;

QY 21 EIVLTQSPGTLSPGERATLSCASQSVYDGSYMNWYQKPGQAPRLIYAASNLES 80
||||| ||||||||||||| : ||| ||||||||||||| ||| |||||||
Db 1 EIVLTQSPGTLSPGERATLSCASQSVYDGSYMNWYQKPGQAPRLIYAASNLES 57

QY 81 GIPDRFSGSGTDTLTISRLEPDAFYVYCOQSNEDPRTFGGQTKLEIKR 132
||||| ||||||||||||| : ||| ||||||||||||| ||| |||||||
Db 58 GIPDRFSGSGTDTLTISRLEPDAFYVYCOQSGSPDTFGGQTKVEIKR 109

RESULT 13

KV3H_HUMAN STANDARD; PRT; 129 AA.
ID KV3H_HUMAN
AC P04207;
DT 20-MAR-1987 (Rel. 04, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION CLL PRECURSOR (RHEUMATOID FACTOR).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86177570; PubMed=3083417;
RA Jirik F.R., Sorge J., Fong S., Heitzmann J.G., Curd J.G., Chen P.P.,
RA Goldfien R., Carson D.A.;
RT "Cloning and sequence determination of a human rheumatoid factor
RT light-chain gene."
RL Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).

CC -----
CC EMBL; M12740; AA58992.1; -.
DR PIR; A01898; K3HUCU.
DR HSP; P01789; 2MCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.

FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION CLL.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
FT DOMAIN 109 118 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 119 129 JK1 SEGMENT.

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FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14275 MW; 5C13B411BE60CC14 CRC64;

Query Match 37.7%; Score 468.5; DB 1; Length 129;
Best Local Similarity 70.7%; Pred. No. 6.7e-32;
Matches 94; Conservative 15; Mismatches 19; Indels 5; Gaps 2;

QY 1 METDTILLWLLVWPSTGEIVLTQSPGRLSLSPGERATLSCRSQSVVDGDSYNNWY 60
DB 1 MEAPAQQLLLWLPDTEIVNTQSPATLSVSPGERATLSCRSQSV-----SNNLAWY 56
QY 61 QOKPQAPRLLIYAASNLESGIPDRFSGSGTDFTLTISRLEPEDFAVYVCOQ-SNEDP 119
DB 57 QOKPQAPRLLIYGASTRAIGTIPARFSGSGTEFTLTISRLEQEDFAVYVCOQINNWP 116
QY 120 RTFGQGTKEIKR 132
DB 117 WTFGGTRVEIKR 129

RESULT 14
KV3E_HUMAN STANDARD; PRT; 109 AA.
AC P01623;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION WOL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT group."
RL Biochemistry 20:5816-5822(1981).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR; A01896; K3HWL.
DR HSSP; P01789; 2MCP.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11746 MW; 566C115E6B9CBEE CRC64;

Query Match 37.4%; Score 464.5; DB 1; Length 109;
Best Local Similarity 82.1%; Pred. No. 1.2e-31;
Matches 92; Conservative 5; Mismatches 12; Indels 3; Gaps 1;

QY 21 EIVLTQSPGTLSPGERATLSCRSQSVVDGDSYNNWYQOKPQAPRLLIYAASNLES 80
DB 1 EIVLTQSPGTLSPGERATLSCRSQSV---SSGILGWYQOKPQAPRLLIYGASSRAT 57
QY 81 GIPDRFSGSGTDFTLTISRLEPEDFAVYVCOQSNEDPRTFGQGTKEIKR 132
DB 58 GIPDRFSGSGTDFTLTISRLEPEDFAVYVCOQYGSILGRTFGQGTKEIKR 109

RESULT 15
KV3L_MOUSE STANDARD; PRT; 111 AA.
ID KV3L_MOUSE
AC P01664;
```

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DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION CBPC 101.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions."
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A01936; KVMSC1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 39 53 FRAMEWORK 2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 61 92 FRAMEWORK 3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 102 111 FRAMEWORK 4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11964 MW; E2BIAD98AD965962 CRC64;

Query Match 37.3%; Score 463; DB 1; Length 111;
Best Local Similarity 79.3%; Pred. No. 1.6e-31;
Matches 88; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 21 EIVLTQSPGTLSPGERATLSCRSQSVVDGDSYNNWYQOKPQAPRLLIYAASNLES 80
DB 1 DIVLTQSPASLAVSLGQRATISCRASQSVDTGESYNNWYQONPQSPKLLIYAASNLES 60
QY 81 GIPDRFSGSGTDFTLTISRLEPEDFAVYVCOQSNEDPRTFGQGTKEIKR 131
DB 61 GIPARFSGSGTDFTLTINHPVEEDAATYYCQSNEDPYTFGGGTKEIKR 111

Search completed: April 17, 2002, 16:41:04
Job time: 172 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 17, 2002, 16:37:52 ; Search time 40.91 Seconds
(without alignments)
850.961 Million cell updates/sec

Title: US-09-499-662-107
 Perfect score: 1242
 Sequence: 1 METDTILLWLLWLLVPGSTG.....EVTHQGLSSPVTKSFNRGEC 238

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues
Total number of hits satisfying chosen parameters: 473505

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

```
Database : SPTREMBL_17.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhmc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Query			DB	ID	Description
			Match	Length				
1	1	757.5	61.0	238	11	Q99M37	Q99m37 mus musculu	
2	2	691	55.6	214	11	Q9RIA5	Q9ria5 mus musculu	
3	3	457.5	36.8	109	4	Q9UL78	Q9ul78 homo sapien	
4	4	434.5	35.0	109	4	Q9UL86	Q9ul86 homo sapien	
5	5	428.5	34.5	235	11	Q99M11	Q99m11 mus musculu	
6	6	410	33.0	108	4	Q9UL77	Q9ul77 homo sapien	
7	7	406	32.7	108	4	Q9UL83	Q9ul83 homo sapien	
8	8	397.5	32.0	109	4	Q9UL85	Q9ul85 homo sapien	
9	9	394	31.7	108	4	Q9UL79	Q9ul79 homo sapien	
10	10	392	31.6	108	4	Q9UL70	Q9ul70 homo sapien	
11	11	380.5	30.6	107	4	Q9UL81	Q9ul81 homo sapien	
12	12	370	29.8	103	11	Q9JL80	Q9jl80 mus musculu	
13	13	367	29.5	114	4	Q9UL80	Q9ul80 homo sapien	
14	14	356.5	28.7	106	5	Q9U410	Q9u410 schistosoma	
15	15	339	27.3	99	11	Q9JL74	Q9jl74 mus musculu	
16	16	339	27.3	107	11	Q9ERZ9	Q9erz9 mus musculu	
17	17	336.5	27.3	104	11	Q9JL82	Q9jl82 mus musculu	
18	18	336	27.1	298	11	Q9QYF0	Q9qyf0 mus musculu	
19	19	328	26.4	97	11	Q9JL76	Q9jl76 mus musculu	

ALIGNMENTS

RESULT 1

Q99M37 PRELIMINARY; PRT; 238 AA.

ID Q99M37
AC Q99M37;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:5947).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY TUMOR;
RA Scrausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002035; AAH02035.1; -;
SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

[illegible]

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RESULT 2
ID Q9RIA5 PRELIMINARY; PRT; 214 AA.
AC Q9RIA5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF152371; AAD40242.1; -.
DR HSP; P01789; IMCP.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_Like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR NON_TER 1
FT NON_TER 214
FT SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

Query Match 55.6%; Score 691; DB 11; Length 214;
Best Local Similarity 59.2%; Pred. No. 2.3e-56;
Matches 129; Conservative 34; Mismatches 51; Indels 4; Gaps 1;

QY 21 EIVLTQSPGTLSPGERATLSCASQSDYDGDSDSYNNWYQKPGQAPRLIIYAASNLES 80
:| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 1 DIQLTQSPSMYASLGERVTITCKASQDI----NSYLSWFOQKPGKPKTLIYRANRLVD 56

QY 81 GIPDRFSGSGGTDFLTISRLEPEFAVYYCQSNEDPRTFGQTKLEIKRTVAAPSVF 140
:| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 57 GVPDRFSGSGGQDYSLTISSELYEDGIYQLYDEFPETFGSGTKLEIKRAAAPTYS 116

QY 141 IFPPSEDLKSGTASVYCLLNNEYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 117 IFPPSEQLTSGGASVCFVFNPNFPKDNVKKIDGSRQGVLSNTDQDSKDSTYSMS 176

QY 201 STLTLSKADYERKHVACEVTHOGLSPVTKSPNRGEC 238
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 177 STLTLPKDEYERNSTYCEATHKTSIPVKCFNRNEC 214

RESULT 3
ID Q9UL78 PRELIMINARY; PRT; 109 AA.
AC Q9UL78;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;

Query Match 35.0%; Score 434.5; DB 4; Length 109;
Best Local Similarity 77.7%; Pred. No. 6.2e-33;
Matches 87; Conservative 6; Mismatches 16; Indels 3; Gaps 1;

QY 21 EIVLTQSPGTLSPGERATLSCASQSDYDGDSDSYNNWYQKPGQAPRLIIYAASNLES 80
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 EIVLTQSPGTLSPGERATLSCASQSV---SSSYLAWYQKPGQAPRLIIYGTSSRAT 57

QY 81 GIPDRFSGSGGTDFLTISRLEPEFAVYYCQSNEDPRTFGQTKLEIKR 132
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 58 GIPDRFSGSGGTDFLTISRLEPEFAVYYCQYQSSPLTFGGTKVKEIKR 109

RESULT 4
ID Q9UL86 PRELIMINARY; PRT; 109 AA.
AC Q9UL86;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;

Query Match 36.8%; Score 457.5; DB 4; Length 109;
Best Local Similarity 81.2%; Pred. No. 4.5e-35;
Matches 91; Conservative 5; Mismatches 13; Indels 3; Gaps 1;

QY 21 EIVLTQSPGTLSPGERATLSCASQSDYDGDSDSYNNWYQKPGQAPRLIIYAASNLES 80
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 EIVLTQSPGTLSPGERATLSCASQSV---SSSYLAWYQKPGQAPRLIIYGTSSRAT 57

QY 81 GIPDRFSGSGGTDFLTISRLEPEFAVYYCQSNEDPRTFGQTKLEIKR 132
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 58 GIPDRFSGSGGTDFLTISRLEPEFAVYYCQYQSSPLTFGGTKVKEIKR 109
```

```
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035036; AAD56272.1; -.
DR HSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR NON_TER 1
FT NON_TER 109
FT SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match 35.0%; Score 434.5; DB 4; Length 109;
Best Local Similarity 77.7%; Pred. No. 6.2e-33;
Matches 87; Conservative 6; Mismatches 16; Indels 3; Gaps 1;

QY 21 EIVLTQSPGTLSPGERATLSCASQSDYDGDSDSYNNWYQKPGQAPRLIIYAASNLES 80
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 EIVLTQSPGTLSPGERATLSCASQSV---SSSYLAWYQKPGQAPRLIIYGTSSRAT 57

QY 81 GIPDRFSGSGGTDFLTISRLEPEFAVYYCQSNEDPRTFGQTKLEIKR 132
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 58 GIPDRFSGSGGTDFLTISRLEPEFAVYYCQYQSSPLTFGGTKVKEIKR 109

RESULT 4
ID Q9UL86 PRELIMINARY; PRT; 109 AA.
AC Q9UL86;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;

Query Match 36.8%; Score 457.5; DB 4; Length 109;
Best Local Similarity 81.2%; Pred. No. 4.5e-35;
Matches 91; Conservative 5; Mismatches 13; Indels 3; Gaps 1;

QY 21 EIVLTQSPGTLSPGERATLSCASQSDYDGDSDSYNNWYQKPGQAPRLIIYAASNLES 80
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 EIVLTQSPGTLSPGERATLSCASQSV---SSSYLAWYQKPGQAPRLIIYGTSSRAT 57

QY 81 GIPDRFSGSGGTDFLTISRLEPEFAVYYCQSNEDPRTFGQTKLEIKR 132
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 58 GIPDRFSGSGGTDFLTISRLEPEFAVYYCQYQSSPLTFGGTKVKEIKR 109
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SQL	SEQUENCE	108 AA; 11738 MW; C06681716C4D16F3 CRC64;
	Query Match	33.0%; Score 410; DB 4; Length 108;
	Best Local Similarity	68.8%; Pred. No. 1.1e-30;
	Matches	77; Conservative 16; Mismatches 15; Indels 4; Gaps
QY	21 EIVLTSPGTLSPGERATLSCKASQSVDYDGDSYMMWYQQKGAPRLLIYAASNLES 80	
Db	: : : : :	
1	DIQMTQPSLSASVGRVTITCRASQSI-----SSLNWYQQKGAPRLLIYAASSLQS 56	
QY	81 GIPDRSGSGCTDFLTISRLEPEDFAVYYCOOSNEDPRTFGGTKLEIKR 132	
Db	: :	
57	GVPFRSGSGCTDFLTISRLEPEDFAVYYCOOSNEDPRTFGGTKRVETIKR 108	
RESULT	7	
Q9ULB3	ID Q9ULB3 PRELIMINARY; PRT; 108 AA.	
AC	Q9ULB3;	
DT	01-MAY-2000 (TREMBLrel. 13, Created)	
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)	
DE	MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).	
OS	Homo sapiens (human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
ON	NCBL_TaxID=9606;	
RX	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=98277139; PubMed=9614934;	
RA	Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,	
RA	Young D.C.;	
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal	
RT	fetus";	
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).	
CC	-I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX	
CC	DOMAIN.	
DR	EMBL; AF035031; AAD56267.1; -.	
DR	HSSP; P01607; IREI.	
DR	InterPro; IPR003006; Ig_MHC.	
DR	InterPro; IPR003596; Ig_V.	
DR	Pfam; PF00047; Ig_1.	
DR	SMART; SM00406; IGv; 1.	
FT	NON_TER 1	
FT	NON_TER 108 108	
SQL	SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;	
	Query Match	32.7%; Score 406; DB 4; Length 108;
	Best Local Similarity	73.2%; Pred. No. 2.7e-30;
	Matches	82; Conservative 9; Mismatches 17; Indels 4; Gaps
QY	21 EIVLTSPGTLSPGERATLSCKASQSVDYDGDSYMMWYQQKGAPRLLIYAASNLES 80	
Db	:	
1	EIVTQSPATLSLSPGERATLSCRASQSV-----SSNLAWYQQKGAPRLLIYCASTRAT 56	
QY	81 GIPDRSGSGCTDFLTISRLEPEDFAVYYCOOSNEDPRTFGGTKLEIKR 132	
Db	:	
57	GIPARFGSGSGCTDFLTISRLEPEDFAVYYCOHYNNPPFTFGTKRVDIKR 108	
RESULT	8	
Q9ULB5	ID Q9ULB5 PRELIMINARY; PRT; 109 AA.	
AC	Q9ULB5;	
DT	01-MAY-2000 (TREMBLrel. 13, Created)	
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)	
DE	MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).	
OS	Homo sapiens (human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	

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RESULT 5
Q99M11 ID Q99M11 PRELIMINARY; PRT; 235 AA.
AC Q99M11;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:6743).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC002129; AAH02129.1;
SQ SEQUENCE 235 AA; 25403 MW; 39807BFE6782A3FB CRC64;

Query Match 34.5%; Score 428.5; DB 11; Length 235;
Best Local Similarity 42.6%; Pred No. 5.9e-32;
Matches 101; Conservative 37; Mismatches 86; Indels 13; Gaps 7;

QY 7 LLWVLLWVFGSTGEIVLTQSPGTLSPGERATLSCAKASQVDYDGDYSYNNWYQQKPGQ 66
Db 6 LLLVFLHLTGSCAQLVLTQ-PSSVSTSLGSTAKLPCKA--STGNIGDSYNNWYQQYNGR 62

QY 67 APRLLIYAASNLGSGIDPRSGS--GGTDETLTIRLEPEDFAVYVYCOQSNEDPRTFGQ 124
Db 63 SPTNMIIYGDLLRPSGSDRFSGSDSSNSAFLTIQNVAQDEADYICQSYSSGIRVEFG 122

QY 125 GKLEI-KRTVAAPSVFTFPSSDQLSGTASVCLLNNFYPREAKYQWKVDNALQSGNS 183
Db 123 GTKLTVLSQPKTSFVILFPSPSELETNKLTVCTISDFPGVTVVDWKADG---TPVT 179

QY 184 QESVTEQDSK--DSTYSLSTLTLSKADYKHKHYACEVTHQGLSSPYTKSFNRGEC 238
Db 180 QGVETTPSQNNKNKYMASSVLTITAKAWETHSSYSCQVTHEG-HIVKSLSRADC 234

RESULT 6
Q9UL77 ID Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98277139; Pubmed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN
DR EMBL: AF035037; AAD56273.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Igv; 1.
FT NON_TER 1
FT NON_TER 108 108

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RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AF035033; AAD56269.1; -.
DR HSP; P80362; IWL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 30.6%; Score 380.5; DB 4; Length 107;
Best Local Similarity 65.2%; Pred. No. 6.1e-28;
Matches 73; Conservative 18; Mismatches 16; Indels 5; Gaps 2;

Qy 21 EIVTQSPGTLSPGERATLSCKASQSDVDGSDYNNWYQKPGQAPRLIIYAASNL 80
Db 1 DIQMTQSPSSLSASVGRVTITCRASQSI-----SNYLNWYQKPGKAPNLLIIYAASLSQS 56

Qy 81 GIPDRFSGSGTDFTLTISRLEPEDFVYVYCOOSNEDPRTFGQTKLEIKR 132
Db 1 GIPDRFSGSGTDFTLTISRLEPEDFVYVYCOOSNEDPRTFGQTKLEIKR 132

Qy 57 GVPDRFSGSGTDFTLTISRLEPEDFVYVYCOOSNEDPRTFGQTKLEIKR 107
Db 57 GVPDRFSGSGTDFTLTISRLEPEDFVYVYCOOSNEDPRTFGQTKLEIKR 107

RESULT 12
Q9JL80 PRELIMINARY; PRT; 103 AA.
AC Q9JL80;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/C;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AF206026; AAF69324.1; -.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 103
SQ SEQUENCE 103 AA; 11224 MW; EC87D653DB3AAB21 CRC64;

Query Match 29.8%; Score 370; DB 11; Length 103;
Best Local Similarity 67.6%; Pred. No. 5.5e-27;
Matches 69; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

Qy 30 TSLSPGERATLSCKASQSDVDGSDYNNWYQKPGQAPRLIIYAASNLGSGIPDRFSGS 89
Db 2 SLAYSLGQRATISCRASEVEYGTGTLQWYQKPGQAPRLIIYAASNLGSGVPAREFSGS 61

Qy 90 GSGTDFTLTISRLEPEDFVYVYCOOSNEDPRTFGQTKLEIKR 131
Db 62 GSGTDFSLNTHPVEEDDIAMFYCOOSRKVPWPTFGGQTKLEIKR 103

RESULT 13
Q9UL80 PRELIMINARY; PRT; 114 AA.
AC Q9UL80;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RC MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AF035034; AAD56270.1; -.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 114
SQ SEQUENCE 114 AA; 12775 MW; 070E31E210D1CB01 CRC64;

Query Match 29.5%; Score 367; DB 4; Length 114;
Best Local Similarity 61.4%; Pred. No. 1.2e-26;
Matches 70; Conservative 21; Mismatches 21; Indels 2; Gaps 2;

Qy 21 EIVTQSPGTLSPGERATLSCKASQSDVDGSDYNNWYQKPGQAPRLIIYAASNL 79
Db 1 DVMTQSPSLPVLTRQPAISICRSPVSDGTYLNWQKPGQAPRLIIYKVSNRD 60

Qy 80 SGIPDRFSGSGTDFTLTISRLEPEDFVYVYCOOSNE-DPRTFGQTKLEIKR 132
Db 61 SGVPDRFSGSGTDFTLTISRLEPEDFVYVYCOOSNE-DPRTFGQTKLEIKR 114

RESULT 14
Q9U410 PRELIMINARY; PRT; 106 AA.
AC Q9U410;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE MONOCLONAL ANTI-IDIDIOTYPIC ANTIBODY NP30 IMMUNOGLOBULIN LIGHT CHAIN
VARIABLE REGION (FRAGMENT).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
OC Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae;
OC Schistosoma.
OX NCBI_TaxID=6182;
RN 1
RP SEQUENCE FROM N.A.
RA Song X.T., Feng Z.O., Qiu Z.N., Li Y.O., Huang H.L., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the light chain
variable region gene of monoclonal anti-idiotypic antibody NP30 of
Schistosoma japonicum.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AF207620; AAF19434.1; -.
DR HSP; P01679; 2FBJ.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
```

	Query Match	27.3%	Score 339;	DB 11;	Length 99;
	Best Local Similarity	64.4%;	Pred. No. 3.9e-24;		
	Matches	65;	Conservative 13;	Mismatches 19;	Indels 4;
	Gaps				1;
QY	31	LSLSGPERATLSCAKASGVDDYDGSYNNWYQOKPQCAPRLIYAASNLGSGIPDFSGSG	90		
		: :			
Db	3	LLVSAGDRVITTCASQSVND----	YAWYQOKPQSPKLLIYASNRYTGVDPDFGSG	58	
QY	91	SGDTFTLTISLRPEDFAVYYCQGSNEDPRTFGGT	KLEIK 131		
		: : :			
Db	59	YGDFTFTISTVQAEDLAVFYCQDYSPPRTFGGTT	KLEIK 99		

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 17, 2002, 16:38:53 ; Search time 40.38 Seconds
(without alignments)
862.171 Million cell updates/sec

Title: US-09-499-662-117
Perfect score: 2517
Sequence: 1 MGWSCIILFLVATATGVHSQ.....MHEALNHVYTKSLSPCK 470

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_1101.*
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
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21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2517	100.0	470	AAW83037	Anti-Fas humanised
2	2517	100.0	470	AA147779	Humanised anti-Fas
3	2517	100.0	470	AAW90929	Humanised HFE7A de
4	2514	99.9	470	AAW90933	Humanised anti-Fas
5	2512	99.8	470	AAW90934	Humanised anti-Fas
6	2511	99.8	470	AAW90935	Humanised anti-Fas
7	2504	99.5	470	AAW83036	Anti-Fas humanised
8	2504	99.5	470	AA147776	Humanised anti-Fas
9	2504	99.5	470	AAW90926	Humanised HFE7A de
10	2498	99.2	470	AAW90936	Humanised HFE7A de
11	2301	91.4	652	AAW48650	Heavy chain of hma

12	2287.5	90.9	465	22	AAW72228	Humanised 323/A3 (
13	2287	90.9	470	21	AAW808026	A dimeric anti-CD2
14	2283	90.7	466	22	AAE03755	Chimeric 2403 IgG
15	2282.5	90.7	464	22	AAW72232	Humanised 323/A3 (
16	2252	89.5	476	20	AAW88464	Monoclonal antibody
17	2248.5	89.3	481	13	AAW24442	Sequence of antiHo
18	2245	89.2	472	20	AAW50166	Human reshaped F19
19	2229	88.6	449	14	AAW43339	Completely humanis
20	2229	88.6	449	19	AAW49816	Anino acid sequenc
21	2227	88.5	476	14	AAW31023	Antibody D heavy c
22	2226.5	88.5	583	22	AAW83156	Ganglioside GM2 an
23	2199.5	87.4	467	22	AAW36210	Human immune syste
24	2197.5	87.3	452	20	AAW29458	Recombinant immuno
25	2137.5	87.3	452	21	AAW30322	Humanised anti-IL-
26	2197.5	87.3	452	21	AAW77766	Humanised anti-IL-
27	2197	87.3	472	20	AAW50157	Chimeric mouse/hum
28	2190	87.0	592	22	AAW83838	Amino acid sequenc
29	2188.5	86.9	452	19	AAW69316	Anti-IL-8 humanise
30	2187	86.9	595	20	AAW86003	Anti-5T4 single ch
31	2185.5	86.8	473	22	AAW84475	Human type antihum
32	2185	86.8	474	22	AAU14177	Human novel protei
33	2182.5	86.7	473	22	AAW64471	Human type antihum
34	2177.5	86.5	473	22	AAW64469	Human type antihum
35	2174	86.4	468	20	AAW85689	D9D10 heavy chain
36	2174	86.4	711	20	AAW85692	MoTABII fusion pro
37	2170.5	86.2	473	22	AAW84473	Human type antihum
38	2159	85.8	470	13	AAW22757	Reshaped CAMPATH-1
39	2157.5	85.7	453	20	AAW50151	Antibody F19 chime
40	2155	85.6	472	17	AAW93166	Anti-rhesus D reco
41	2152.5	85.5	454	14	AAW30774	H52H4-160 murine a
42	2146.5	85.3	467	13	AAW22758	Reshaped CD4 antib
43	2142.5	85.1	467	13	AAW22759	Reshaped CD4 antib
44	2142.5	85.1	477	22	AAU14288	Human novel protei
45	2139	85.0	466	14	AAW40750	Sequence encoded b

ALIGNMENTS

RESULT	1
AAW83037	
ID	AAW83037 standard; Protein; 470 AA.
XX	
AC	AAW83037;
XX	
DT	15-MAR-1999 (first entry)
XX	
DE	Anti-Fas humanised antibody HFE7A heavy chain.
XX	
KW	HFE7A; monoclonal antibody; mouse; Fas; humanised antibody; apoptosis; HFE7A; autoimmune disease; Hashimoto's disease; systemic lupus erythematosus; graft versus host disease; Sjogren syndrome; pernicious anaemia; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy.
XX	
OS	Homo sapiens.
XX	
OS	Synthetic.
XX	
Key	Location/Qualifiers
FT	1..19
FT	Peptide
FT	/label= Sig_peptide
FT	20..470
FT	Protein
FT	/label= Mat_protein
FT	20..140
FT	Region
FT	/label= Variable
FT	141..464
FT	Region
FT	/label= Constant

CC the treatment or prevention of conditions such as autoimmune diseases,
CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
CC and organ graft rejection. Sequences AAB14775-B14776 and AAB14779
CC represent the heavy chains (or fragments thereof) of various humanised
CC HFE7A-derived anti-Fas antibodies.
XX
SQ Sequence 470 AA;

Query Match 100.0%; Score 2517; DB 21; Length 470;
Best Local Similarity 100.0%; Pred. No. 9.2e-145;
Matches 470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGVSCIIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVKQAP 60
Db 1 mgwsciiilflvatatgvhsqvlvqsgaevkpgasvkvsckasgytftsywmqvkkqap 60

Qy 61 GGLGEMWGEIDPSDSYTNVYNOKFKGKATLTVDSTSTAYMELSSLSRSEDVAVYVCARNRD 120
Db 61 ggglewmgeidpsdsytnynqkfkgkatltvdststaymelslsrsedtavvycarnrd 120

Qy 121 YSNNNYFDVWVGSGTTLVTSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVYS 180
Db 121 ysnnyfvdwvgsgtltvssastkgpsvfplapskstsggtaalgclvkdypfpptvys 180

Qy 181 WNSGALTSGVHTFPVAVLQSSGLYSLSVVVTPSSSLGTQTYICNVNHHKPSNTKVDKRVEP 240
Db 181 wnsгалtsгvhtfpavlqssglyslsvvtpssslgtqtyicnvnhkpсntkvdkrvep 240

Qy 241 KSCDKTHCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
Db 241 kscdkthcpcpapeilggpsvflfppkpkdtlmsrtpevtcvvvdvshedpevkfnw 300

Qy 301 YVDGVEVHNAKTPREQYNSTYRVVSVLTVHLQDVLNGKEYCKVKSNKALPAPIEKTTIS 360
Db 301 yvdgvevhnaktpreeqynstyrvvsvltvhlqdvlngkeyckvksnkalpapiektis 360

Qy 361 KAKGPDPREQVYTLPPSREMTKNOVSLTCLVKGYPSPDIQVAVESNQGPENNYKTPPV 420
Db 361 kagdprepqvtylppsremtknvstclvkgypspdiqvavessngqpennyyktppv 420

Qy 421 LNSDGSFFLYSKLTVDKSRMQGNVFCSCVMHEALHNHYTKLSLSLSPGK 470
Db 421 lnsdgsfflyskltvdksrmqgnvfscsvmhеalhnhytklslspsgk 470

RESULT 3
AAW90929
ID AAW90929 standard; Protein; 470 AA.

AC AAW90929;
XX
DT 08-AUG-2000 (first entry)
XX
DE Humanised HFE7A designed heavy chain protein #2.

XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;
KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
KW nephrotropic; antifertility; neuroprotective; antiatherosclerotic;
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KW Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;
KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
XX Synthetic.
OS
XX EP990663-A2.
PN
XX

PD 05-APR-2000.
XX
PF 29-SEP-1999; 99EP-0307711.
XX
PR 30-SEP-1998; 98JP-0276881.
PR 30-SEP-1998; 98JP-0276882.
XX
PA (SANY) SANKYO CO LTD.
XX
PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
XX
DR WPI: 2000-258930/23.
DR N-PSDB; AAA11622.
XX
PT New humanized anti-Fas antibody, useful for treating or preventing e.g.
PT inflammatory or autoimmune disease, induces apoptosis selectively in
PT cells with abnormal Fas-Fas ligand systems -
PS Example reference 22; Page 150-152; 263pp; English.
XX
CC This invention describes a novel humanized anti-Fas antibody-like
CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
CC ligand system, by binding to Fas on the cell surface, and prevents
CC apoptosis in cells with a normal system, by inhibiting binding between
CC Fas and its ligand. The products of the invention have anti-inflammatory,
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
CC antirheumatic, nephrotropic, antifertility, neuroprotective,
CC antiatherosclerotic, cardiac and hepatotropic activity. (I) induce
CC apoptosis by binding to cell surface Fas or inhibit it by competitive
CC inhibition of ligand binding. (I) are used to treat and/or prevent
CC diseases associated with the Fas/Fas ligand system, especially systemic
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
CC inhibit apoptosis in normal cells but selectively induce it in abnormal
CC cells. They bind to both human and murine Fas, so can be evaluated in
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
CC the native ligand, do not induce liver disease, and have reduced risk of
CC inducing a human anti-murine antibody response. This sequence represents
CC a humanised anti-Fas antibody HFE7A designed heavy chain which is used in
CC the method described in the invention.
XX
SQ Sequence 470 AA;

Query Match 100.0%; Score 2517; DB 21; Length 470;
Best Local Similarity 100.0%; Pred. No. 9.2e-145;
Matches 470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGVSCIIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVKQAP 60
Db 1 mgwsciiilflvatatgvhsqvlvqsgaevkpgasvkvsckasgytftsywmqvkkqap 60

Qy 61 GGLGEMWGEIDPSDSYTNVYNOKFKGKATLTVDSTSTAYMELSSLSRSEDVAVYVCARNRD 120
Db 61 ggglewmgeidpsdsytnynqkfkgkatltvdststaymelslsrsedtavvycarnrd 120

Qy 121 YSNNNYFDVWVGSGTTLVTSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVYS 180
Db 121 ysnnyfvdwvgsgtltvssastkgpsvfplapskstsggtaalgclvkdypfpptvys 180

Qy 181 WNSGALTSGVHTFPVAVLQSSGLYSLSVVVTPSSSLGTQTYICNVNHHKPSNTKVDKRVEP 240
Db 181 wnsгалtsгvhtfpavlqssglyslsvvtpssslgtqtyicnvnhkpсntkvdkrvep 240

Qy 241 KSCDKTHCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
XX

Db 241 kscdkthtccpccpapellgpgsvflfppkpkdtlmisrtpevtcvvvdshdpevkfnw 300
 QY 301 YVDGVEVHNKATKPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIERTIS 360
 Db 301 yvdgvevhnaktkpreeqynstyrsvsvltvlhqdwingkeyckvsnkalpapiertis 360
 QY 361 KAKQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEESGQPENNYKTTPPV 420
 Db 361 kagqprepqvytlppsreemtknqvaltclvkgyfypsdiavevesngqpennykttppv 420
 QY 421 LDSGSPFLYSKLTVDKSRWQGNVFCSCVMHEALHNYTKQSLSPGK 470
 Db 421 ldsdgsfllyskltvdksrwqgnvfscsvmhealhhnytkqslspgk 470

RESULT 4
 AAW90933
 ID AAW90933 standard; Protein; 470 AA.
 AC AAW90933;
 XX 08-AUG-2000 (first entry)
 DT Humanised anti-Fas designed heavy chain Heu 1 protein.
 DE
 XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 KW dermatologic; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 XX Synthetic.
 OS
 XX EP990663-A2.
 PN
 XX 05-APR-2000.
 PD
 XX 29-SEP-1999; 99EP-030711.
 PF
 XX 30-SEP-1998; 98JP-0276881.
 PR 30-SEP-1998; 98JP-0276882.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 XX WPI; 2000-258930/23.
 DR N-PSDB; AAA11644.
 DR

PT New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems
 XX
 XX Claim 2; Page 169-170; 263pp; English.
 PS
 XX This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatologic, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic

CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody heavy chain construct designated Heu 1
 CC which is described in the method of the invention.
 XX
 SQ Sequence 470 AA;

Query Match 99.9%; Score 2514; DB 21; Length 470;
 Best Local Similarity 99.8%; Pred. No. 1.4e-144;
 Matches 469; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGWSCIIILFVATATGVHSQVLVQSGAEVKKPGASVKVSKASGYTFTSYMMQWVKQAP 60
 Db 1 mgwsciiilfvatatgvhsqvlvsgaevkpgasvkvsckasgytftsymbwvkqap 60
 QY 61 GQGLEWNGEIDPDSYNYNOKFKGKATLVDTSTSTAYMELSSLRSEDFAVYCARNRD 120
 Db 61 gqglewngeidpdsy cynyngkfkgkatltvdtststaymelslsrseidtavycarnrd 120
 QY 121 YSNWYDFVMGEGFLTVSVSASTKGPSVFLAPSKSTSGTAAALGCLVKDYFPEPTVTS 180
 Db 121 ysnwdfvmgegfltvsvsastkgpsvflapskstsgtgaalgcclvkdyfpeptvts 180
 QY 181 WNSGALTSVGHVTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICWNHKKPSNKKVDRKVEP 240
 Db 181 wnsгалtsvghvtfpavliqssglyslssvvtvpssslgtqtyicwnhkkpsnkvdrkvep 240
 QY 241 KSCDKTHTCCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
 Db 241 kscdkthtccpccpapellgpgsvflfppkpkdtlmisrtpevtcvvvdshdpevkfnw 300
 QY 301 YVDGVEVHNKATKPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIERTIS 360
 Db 301 yvdgvevhnaktkpreeqynstyrsvsvltvlhqdwingkeyckvsnkalpapiertis 360
 QY 361 KAKQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEESGQPENNYKTTPPV 420
 Db 361 kagqprepqvytlppsreemtknqvaltclvkgyfypsdiavevesngqpennykttppv 420
 QY 421 LDSGSPFLYSKLTVDKSRWQGNVFCSCVMHEALHNYTKQSLSPGK 470
 Db 421 ldsdgsfllyskltvdksrwqgnvfscsvmhealhhnytkqslspgk 470

RESULT 5
 AAW90934
 ID AAW90934 standard; Protein; 470 AA.
 XX
 XX AAW90934;
 XX 08-AUG-2000 (first entry)
 DT Humanised anti-Fas designed heavy chain Heu 2 protein.
 DE
 XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 KW dermatologic; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;

CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatologic, immunosuppressive, thymic, antirheumatic,
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic). And transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody heavy chain construct designated Heu 3
 CC which is described in the method of the invention.

xx Sequence 470 AA;

Query Match 99.8%; Score 2511; DB 21; Length 470;
 Best Local Similarity 99.6%; Pred. No. 2.1e-144;
 Matches 468; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGWSCILFLVATATGVHSGVQLVQSGAEVKKPGASVKVSCKASGYTFSTYWMQVQKAP 60
 Db {|||||}|||||}|||||}|||||}|||||}|||||}|||||}|||||}|||||}|||||}
 1 mgwscillflvatatgvhsgvqlvqsgaevkpgasvkvsckasgytftsymqwrqap 60
 Qy 61 GQGLEWNGEIDPDSYNNYNGKFKGKATLTVDSTSTAYMELSLRSEDATVAYTCARNRD 120
 Db {|||||}|||||}|||||}|||||}|||||}|||||}|||||}|||||}|||||}
 61 gqglewngeidpsdsytnyngkfkgtatltvdststaymelslrsedatvayycarnrd 120
 Qy 121 YSNWNYFDVWCEGTLVNVSSASTGPSVFPLAPSSKSTSGGTAALGCLVKDPFPEPTVTS 180
 Db {|||||}|||||}|||||}|||||}|||||}|||||}|||||}|||||}|||||}
 121 ysnwnyfdvvgqgltlvntssastgpsvfplapsskstsggtaalgclvkdfpfpvtvts 180
 Qy 181 WNSGALSGVHTFPVAVLQSSGLYSLSVVVTPVSSSLGTQTYICNVNKKPSNTKVDKRVPE 240
 Db {|||||}|||||}|||||}|||||}|||||}|||||}|||||}|||||}|||||}
 181 wnsгалtsгvhtfpavlgssglyslsvvtvpssslgtqtyicnvnhkpsntkvdkrvpe 240
 Qy 241 KSCDKHTCCPCPAPELLGSGPVFLFPKPKDTHMISRTPEVTCVVDVSHEDPEVKFNW 300
 Db {|||||}|||||}|||||}|||||}|||||}|||||}|||||}|||||}|||||}
 241 kscdkhtccpcpapelgsgpvflfpkpkdthmisrtpevtcvvdrvshedpevkfnw 300
 Qy 301 YVDGVEVHNKATKPREQYNSTYRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTIS 360
 Db {|||||}|||||}|||||}|||||}|||||}|||||}|||||}|||||}|||||}
 301 yvdgvevhnaktpreeqynstyrsvsltlvlhqdwingkeyckvsnkalpapiektis 360
 Qy 361 KAKQPREPQVYTLPPGREEMTKNQVSLTCLVKGFYPSDIAVEHESGQPNNYKTTTPPV 420
 Db {|||||}|||||}|||||}|||||}|||||}|||||}|||||}|||||}|||||}
 361 kagqprepqvtytlppgreemtknqslclvklgfypsdiavevesngqpennykttppv 420
 Qy 421 LDSGSEFLYSKLTVDKSRQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 470
 Db {|||||}|||||}|||||}|||||}|||||}|||||}|||||}|||||}|||||}
 421 ldsdgsflfyskltvdksrqoggnvfscsvnhealhnhytqkslsispgk 470

RESULT 7
 AAW83036
 ID AAW83036 standard; Protein: 470 AA.
 XX
 AC AAW83036;
 DT
 XX 15-MAR-1999 (first entry)
 XX

DE Anti-Fas humanised antibody HFE7A heavy chain.
 xx HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
 KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
 KW systemic lupus erythematosus; graft versus host disease;
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 KW transplant rejection; therapy.
 xx Homo sapiens.
 OS Synthetic.
 OS
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Protein /label= Sig_peptide
 FT Region /label= Mat_protein
 FT Region 20..140
 FT Region /label= Variable
 FT Region 141..464
 FT Region /label= Constant
 FT Region 50..54
 FT Region /label= CDR_H1
 FT Region /note= "claim 9"
 FT Region 69..84
 FT Region /label= CDR_H2
 FT Region /note= "claim 9"
 FT Region 118..129
 FT Region /label= CDR_H3
 FT Region /note= "claim 9"
 xx AU9859701-A.
 xx 08-OCT-1998.
 xx 30-MAR-1998; 98AU-0059701.
 xx 08-OCT-1997; 97JP-0276064.
 xx 01-APR-1997; 97JP-0082953.
 xx 25-JUN-1997; 97JP-0169088.
 xx (SANY) SANKYO CO LTD.
 xx Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
 xx Masahiko O, Nobufusa S, Shin Y, Tohru T;
 xx WPI; 1998-543440/47.
 xx N-PSDB; AAV70079.
 xx
 xx New antibodies and proteins bind conserved epitope of Fas antigen -
 xx used to evaluate drugs in animal models and to treat Fas-associated
 xx diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 xx myocarditis, hepatitis and AIDS
 xx
 xx Claim 22; Page 212-213; 292pp; English.
 xx
 xx This is the amino acid sequence of the VD type humanised heavy
 xx chain of murine anti-human Fas monoclonal antibody HFE7A. E. coli
 xx pGHSI7A62 SANK 73397 harbors plasmid pGHSI7A62 carrying a fusion
 xx fragment of the humanised VD type HFE7A heavy chain and DNA
 xx encoding human IgG1 constant region (see AAV70079), and is deposited
 xx as FERM BP-6074 (claimed). The invention provides methods for
 xx producing humanised antibodies by culturing host cells. Humanised
 xx versions of HFE7A (see AAW83031-37), like native HFE7A, are capable
 xx of inducing apoptosis in abnormal cells expressing Fas, and of
 xx inhibiting Fas-induced apoptosis in normal cells. The humanised
 xx antibodies are used to evaluate, in animal models, treatments of
 xx diseases that involve Fas/Fas ligand interactions, and also to

CC treat such diseases, including autoimmune disease (e.g. systemic
CC lupus erythematosus, Hashimoto's disease, graft versus host disease,
CC Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma,
CC autoimmune haemolytic anaemia, Crohn's disease, rheumatoid arthritis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura and
CC insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).
XX
SQ Sequence 470 AA;
Query Match 99.5%; Score 2504; DB 19; Length 470;
Best Local Similarity 99.6%; Pred. No. 5.7e-144;
Matches 468; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MGWSCIIILFLVATATGVHSGVQLVQSGAEVKKPGASVKVSCKRSGYFTFSYMQWVKQAP 60
DB 1 mgwsciiilflvatatgvhsqvlvqsgaevkpgasvkvsckasgyftfsymwvkvqap 60
QY 61 GQGLEWGMGIDSDSYNTYNNQKFKGKATLTVDFTSTAYMELSSLRSEDTAVYYCARNRD 120
DB 61 gqglewmgidpsdsyntynqkfkgtatltvdtstasaymelsslrse dtavyy carnrd 120
QY 121 YSNWYFDVWGEGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKKDYFPEPTVS 180
DB 121 ysnwyfdvwgegl tvtvssastk gpsvfpplapssk stsggtaalgclv kkyfpeptvs 180
QY 181 WNSGALTSVGHFTPPAVLQSSGLYSLSVVTVPPSSSLGTQTYICNVNHNKPSNTKVDKRVPE 240
DB 181 wnsгалtsvghftppav lqssglsyls svvtpvps slgtotyicnv nhnkpsntkvdkrvpe 240
QY 241 KSCDKTHTCCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
DB 241 kscdkthtccpcpapell ggpsvflfppkpkdtlmisrtpevtcvvvdvsh edpevkfnw 300
QY 301 YVDGVEVHNNAKTPREEQYNSTYRVVSVLTVTLHODWLNCKEYKCKVSNKALPAPIEKTIS 360
DB 301 yvdgvevhnna ktpreeqynst yrvvsvltv tlhqdwnl nckeykckvsnkalpapiektis 360
QY 421 LDSGGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 470
DB 421 ldsdgsfflyskltvdksrw qgnvfscsvmheal hnhytqksls spgk 470
RESULT 8
AAB14776
ID AAB14776 standard; Protein; 470 AA.
XX
AC AAB14776;
XX
DT 24-NOV-2000 (first entry)
XX
DE Humanised anti-Fas antibody heavy chain, SEQ ID NO:89.
KW murine; humanised antibody HFE7A; PERM-BP-5828;
KW human Fas; Fas ligand; complementarity determining region; CDR;
KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis;
KW hepatitis; AIDS; graft rejection; heavy chain.
XX
OS Chimeric - Mus musculus.
OS Chimeric - Homo sapiens.
XX
FN JP2000169393-A.
XX
PD 20-JUN-2000.

XX 30-SEP-1999; 99JP-0278301.
XX 30-SEP-1998; 98JP-0276883.
XX (SANY) SANKYO CO LTD.
XX WPI: 2000-485645/43.
DR N-PSDB; AAA72159.
XX
PT Preventive or treating agent for the diseases caused by an abnormality
PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains
PT anti-Fas antibody
XX
PS Claim 21; Page 95-96; 139pp; Japanese.
XX
CC The invention relates to compositions for the prevention or treatment
CC of diseases caused by an abnormality in the Fas/Fas ligand system
CC containing an anti-Fas antibody as the active component. The anti-Fas
CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
CC or a humanised version of HFE7A containing identical CDRs
CC (complementarity determining regions) to antibody HFE7A. Via its
CC interaction with Fas, the antibody of the invention acts as a modulator
CC of apoptosis. The composition of the invention may therefore be used in
CC the treatment or prevention of conditions such as autoimmune diseases,
CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
CC and organ graft rejection. Sequences AAB14775-B14776 and AAB14779
CC represent the heavy chains (or fragments thereof) of various humanised
CC HFE7A-derived anti-Fas antibodies.
XX
SQ Sequence 470 AA;
Query Match 99.5%; Score 2504; DB 21; Length 470;
Best Local Similarity 99.6%; Pred. No. 5.7e-144;
Matches 468; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MGWSCIIILFLVATATGVHSGVQLVQSGAEVKKPGASVKVSCKRSGYFTFSYMQWVKQAP 60
DB 1 mgwsciiilflvatatgvhsqvlvqsgaevkpgasvkvsckasgyftfsymwvkvqap 60
QY 61 GQGLEWGMGIDSDSYNTYNNQKFKGKATLTVDFTSTAYMELSSLRSEDTAVYYCARNRD 120
DB 61 gqglewmgidpsdsyntynqkfkgtatltvdtstasaymelsslrse dtavyy carnrd 120
QY 121 YSNWYFDVWGEGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKKDYFPEPTVS 180
DB 121 ysnwyfdvwgegl tvtvssastk gpsvfpplapssk stsggtaalgclv kkyfpeptvs 180
QY 181 WNSGALTSVGHFTPPAVLQSSGLYSLSVVTVPPSSSLGTQTYICNVNHNKPSNTKVDKRVPE 240
DB 181 wnsгалtsvghftppav lqssglsyls svvtpvps slgtotyicnv nhnkpsntkvdkrvpe 240
QY 241 KSCDKTHTCCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
DB 241 kscdkthtccpcpapell ggpsvflfppkpkdtlmisrtpevtcvvvdvsh edpevkfnw 300
QY 301 YVDGVEVHNNAKTPREEQYNSTYRVVSVLTVTLHODWLNCKEYKCKVSNKALPAPIEKTIS 360
DB 301 yvdgvevhnna ktpreeqynst yrvvsvltv tlhqdwnl nckeykckvsnkalpapiektis 360
QY 361 KAKGQPREQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPV 420
DB 361 kagqpreqv tylppsreemtknq vsltclvk gfypsdi avewesngqpennyk tppv 420
QY 421 LDSGGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 470
DB 421 ldsdgsfflyskltvdksrw qgnvfscsvmheal hnhytqksls spgk 470
RESULT 9
AAB90926

XX	
PI	Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
XX	WPI: 2000-258930/23.
DR	N-PSDB; AA11655.
DR	
XX	New humanized anti-Fas antibody, useful for treating or preventing e.g.
PT	inflammatory or autoimmune disease, induces apoptosis selectively in
PT	cells with abnormal Fas-Fas ligand systems -
XX	
PS	Claim 2; Page 188-189; 263pp; English.
XX	
CC	This invention describes a novel humanized anti-Fas antibody-like
CC	molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
CC	ligand system, by binding to Fas on the cell surface, and prevents
CC	apoptosis in cells with a normal system, by inhibiting binding between
CC	Fas and its ligand. The products of the invention have anti-inflammatory,
CC	anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
CC	immunomodulatory, dermatological, immunosuppressive, thyromimetic,
CC	antirheumatic, nephrotropic, antifertility, neuroprotective,
CC	antiartherosclerotic, cardiact and hepatotropic activity. (I) induce
CC	apoptosis by binding to cell surface Fas or inhibit it by competitive
CC	inhibition of ligand binding. (I) are used to treat and/or prevent
CC	diseases associated with the Fas/Fas ligand system, especially systemic
CC	lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
CC	versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
CC	anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC	disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC	multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
CC	dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
CC	cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
CC	(A, C or B) or alcoholic), and transplant rejection. (I) selectively
CC	inhibit apoptosis in normal cells but selectively induce it in abnormal
CC	cells. They bind to both human and murine Fas, so can be evaluated in
CC	murine disease models. (I) act on the active site of Fas, i.e. they mimic
CC	the native ligand, do not induce liver disease, and have reduced risk of
CC	inducing a human anti-murine antibody response. This sequence represents
CC	a humanised anti-Fas antibody HFE/A heavy chain construct HHH type
CC	which is described in the method of the invention.
XX	
Sequence	470 Aa:
XX	

Query Match	99.2%	Score	2498;	DB	21;	Length	470;
Best Local Similarity	98.9%;	Pred. No.	1.3e-143;				
Matches	465;	Conservative	3;	Mismatches	2;	Indels	0;
						Gaps	0;
QY	1	MGWSCIILFLIVATATGVHSQVLVQSGAEFKKPGASVKVSKCKASGYFTSTWQMWRKQAP	60				
Db	1	mgwscilflivatatgvhsqvlvqsgaeavkpgasvkvsckasgyfttsymwqwrqap	60				
QY	61	GGLEWMGETDPDSSTNYNQKFKGKATLTVDTSTSTAYMELSSLRSEDATVAYVCARNRD	120				
Db	61	ggglewmgetdpdsosyynyqkfgrvltlrtdststaymelslrseadtavycarnrd	120				
QY	121	YSNNWFDVMWEGTFLTVSSASTGSPVFLAPSSKSTSGCTAALGCLVKDYFPEPTVTS	180				
Db	121	ysnnwfdvmwegtfltvssasatkpsvflapsskstsggtaalgclvkdypcptvts	180				
QY	181	WNSGALTSGVHTTPAVILQSSGLYSLSWTVVPSSSLGTQTYICNVNHNKPSNTKVDKRVPE	240				
Db	181	wnsгалtsгvhtfpavilqssgylslswtvvpssslgtqtyicnvhnkpsntkvdkrvpe	240				
QY	241	KSCDKHTTCCPPCAPELILGCPSVFLFPKPKDITLMIIRSTPEVTCCVVVDVSHEDDEVKFNW	300				
Db	241	kscdkhttcpcpapelilgcpsvflfpkpkdtlmiirstpevtccvvvdvshedpevkfnw	300				
QY	301	YVPGVEVHNAKTPREEQYNSTYRVWSVLTVLHODWLNGKRYCKCVSNKALPAPIEKTIS	360				
Db	301	yvdgvevhnaktpreeqynstyrzrvsvltrlhqdwlngkeyckcvsnkalpapielctis	360				
QY	361	KAKGQREPPQYTLPPPSREEMTKNOVSLTCLVKGFPSPDIAYVENSGQPNNTKTTTPPV	420				

[illegible]

Db 1 mdwtvrvfcllavapaghsqvlvqsgaevkkgasvkvskcasgytftshmhvrrqap 60
QY 61 GQLEWMEIDPDSYTNQKFKGKATLVDTSTAYMELSLRSDDTAVYICARNRD 120
Db 61 gqglewgefnpnsgtrnynekfkskatmtvtstntaymelslrsddtavyica-srd 119
QY 121 YS-NNWYFDVWGEGLTVVSS-----ASTKGPSVPPAPSS 155
Db 120 ydydgrfydgwggclvtvssgewilcawaqlcptprshgttslaastkgspsvflapss 179
QY 156 KSTSGGTAALGCLVKDYFPEPTVWSNNGALTSGVHFFPAVLQSSGLYSLSSVTVLPSSS 215
Db 180 kstsggtaalgclvkdypfpvptvwsnsgaltsgvhlfpavlgsglyslssvvtvpss 239
QY 216 LGQTYICNVNHNKPSNTKVDKRVKPKCDKTHTCPPCAPPELLGGPSVFLFPPPKDPTLM 275
Db 240 lgtqtyicnvnhkpsntckvdkvpekscdkthtcppcapellggpsvflfppkpkdtlm 299
QY 276 ISRTPEVTCVVDVSHEDPEVKFNWYDGEVHNHNAKTPREEQYNSTYRVVSVLTVLHQD 335
Db 300 isrtpevtcvvdvshdpevkfnwydgvvhnaktkpreegynstyrvvsvltvlhqd 359
QY 336 WLNGKEYCKVSKNKAAPLPAETKISKAKGQPREPQVYTLPPSRREMTKNQVSLTCLVKGF 395
Db 360 wlngkeyckvsknkalpapietkiskakgprepqvylppsrdeltknqvsltclvkgf 419
QY 396 YPSDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSSVMHEAL 455
Db 420 ypsdiawesngopennyktttvpldsdgsfflyskltvdksrwqgnvfscsvmheal 479
QY 456 HNHYTQKSLSLSPGK 470
Db 480 hnhytqkslspsgk 494

RESULT 12

AAB72228
ID AAB72228 standard; Protein: 465 AA.

XX
AC AAB72228;

XX
DT 10-MAY-2001 (first entry)

XX
DE Humanised 323/A3 (IgG1) antibody heavy chain amino acid sequence.

XX
KW Anti-Ep-CAM antibody; cyclic adenosine monophosphate; cell synthesis;
KW chemotherapeutic agent; cytostatic; anti-cancer therapy; cancer;
XX heavy chain.

XX
OS Mus sp.
XX Homo sapiens.

XX
PN WO200107082-A1.

XX
PD 01-FEB-2001.

XX
PF 23-JUL-1999; 99WO-EP05271.

XX
PR 23-JUL-1999; 99WO-EP05271.

XX
PA (GLAX) GLAXO GROUP LTD.

XX
PI Knick VC, Stimmel JB, Thurmond LM;

XX
DR WPI; 2001-182729/18.

XX
DR N-PSDB; AAF63374.

XX
PT Combination for treating cancer (e.g. breast, gastric or prostate
PT cancers), or in the manufacture of a medicament for anti-cancer
PT therapy, comprises an anti-Ep-cyclic adenosine monophosphate antibody
PT with a chemotherapeutic agent -
XX
XX

PS Disclosure; Fig 16; 103pp; English.

XX

CC This invention relates to a combination of an anti-Ep-CAM (cyclic
CC adenosine monophosphate) antibody with a chemotherapeutic agent, that is
CC capable of arresting Ep-CAM antigen expressing cells in the synthesis (S)
CC phase or the second growth phase (M) of cell enlargement (G2)/DNA
CC replication. The antibody exhibits cytostatic activity and is useful in
CC the manufacture of a medicament for use in anti-cancer therapy,
CC characterised in that a chemotherapeutic agent, which is capable of
CC arresting Ep-CAM antigen expressing cells in S or in G2/M, is
CC co-administered to a patient with an anti-Ep-CAM antibody. The
CC combination is useful for treating cancer, particularly colorectal
CC cancer, breast cancer, gastric cancer, prostate cancer or non-small-cell
CC lung cancer. The present sequence represents the heavy chain of
CC anti-Ep-CAM antibody known as humanised 323/A3 (IgG1) which can be used
CC in the combination of the invention.

XX Sequence 465 AA;

Query Match 90.9%; Score 2287.5; DB 22: Length 465;
Best Local Similarity 91.7%; Pred. No. 6.9e-131;
Matches 431; Conservative 14; Mismatches 20; Indels 5; Gaps 2;

QY 1 MGWSCIIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVKQAP 60
Db 1 mgwsciiilflvatatgvhsqvlvqsgvpevkkpgasvkvskcasgytftnmgmwwrqp 60

QY 61 GQLEWMEIDPDSYTNQKFKGKATLVDTSTAYMELSLRSDDTAVYICARNRD 120
Db 61 gqglewmgwintypteptgyedfkgrfaisldtastaymelslrsddtavyicar--- 117

QY 121 YSNWYFDVWGEGLTVVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180
Db 120 ysnwyfdvwmgeglvtvssastkgpsvfpplapsskstsggtaalgclvkdypfpvptvs 175

QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGFTQTYICNVNHNKPSNTKVDKRV 240
Db 180 wnsaltsgvhtfpavliqssglyslssvtpvpssslgtqtyicnvnhkpsntkvdkkvpe 235

QY 241 KSCDKTHTCPPCAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVDVSHEDPEVFNW 300
Db 240 kscdkthtcppcapellggpsvflfppkpkdtlmisrtpevtcvvdvshdpevkfnw 295

QY 301 YVDGVEVHNARTKPREEQYNSTYRVVSVLTVLHQDLNGLKEYCKVSKNKAAPLPAETKIS 360
Db 300 yvdgvevhnartkpreeqynstyrvvsvltvlhqdnglkeyckvsknkalpapietkis 355

QY 361 KAKGQPREPQVYTLPPSRREMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPV 420
Db 360 kagqprepqvylppsrremtknqvsltclvkgfypsdiavewesngqpennykttppv 415

QY 421 LDSGSPFLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSPGK 470
Db 416 ldsdgsfplyskltvdksrwqgnvfscsvmhealhnhytqkslspsgk 465

RESULT 13

AAB08026

ID AAB08026 standard; Protein: 470 AA.

XX
AC AAB08026;

XX
DT 14-NOV-2000 (first entry)

XX
DE A dimeric anti-CD20 heavy chain polypeptide.

XX
KW Anti-CD20 antibody; dimeric immunoglobulin; immunoglobulin; IgG;
KW complement system; Fc gamma receptor; cytotoxic effector cell;
KW host immune cell; programmed cell death; allergic disorder; cancer;
KW autoimmunity disease; allergic asthma; atopic dermatitis; Crohn's disease;
KW allergic bronchopulmonary aspergillosis; allergic rhinitis;
KW Graves's disease; food allergy; allergic contact dermatitis; cancer;
KW B-cell lymphoma; rheumatoid arthritis; ulcerative colitis; psoriasis;

KW pigeon breeder's disease; hepatitis; leprosy; Lyme disease;
 KW diabetes mellitus; candidiasis; aplastic anaemia.
 XX
 OS Chimeric - Mus sp.
 OS Chimeric - Homo sapiens.
 PH
 PH Key Location/Qualifiers
 FT Peptide 1..19
 FT Protein /note= "signal peptide"
 FT 20..140
 FT /note= "murine anti-human CD20 heavy chain variable
 FT region"
 FT Protein 141..470
 FT /note= "human gamma 1 heavy chain constant region"
 XX
 PN WO200044788-A1.
 XX
 PD 03-AUG-2000.
 XX
 PD 28-JAN-2000; 2000WO-US01893.
 PF
 PF 28-JAN-1999; 99US-0238741.
 PR
 XX (IDEC-) IDEC PHARM CORP.
 XX
 PI Braslawsky GR, Hanna N, Hariharan K, Labarre MJ, Huynh TB;
 XX
 DR WPI; 2000-514811/46.
 DR N-PSDB; AAA63531.
 XX
 PT Genetically engineering immunoglobulin (Ig) G/IgG dimers for the
 PT treatment of cancers, allergic disorders and autoimmune conditions -
 XX
 PS Example 1; Fig 2A-C; 65pp; English.
 XX
 CC The present sequence represents a dimeric anti-CD20 light chain
 CC polypeptide. The dimeric immunoglobulin is used in the method of the
 CC invention. The specification describes a method for producing an
 CC immunoglobulin (Ig) G/IgG dimer. The method comprises genetically
 CC engineering a monoclonal antibody to introduce a cysteine molecule
 CC which inhibits formation of intramolecular disulphide bridges between
 CC sister heavy chains on the same antibody molecule. The dimer is a
 CC homodimer or heterodimer that is capable of activating components of the
 CC complement system, and has the ability to activate and kill cells via the
 CC complement cascade. The dimer is also capable of binding to Fc gamma
 CC receptors on cytotoxic effector cells and on host immune cells, and is
 CC capable of initiating programmed cell death. The IgG/IgG dimers may be
 CC used to treat allergic disorders, cancers and autoimmune diseases such
 CC as allergic asthma, allergic bronchopulmonary aspergillosis, allergic
 CC rhinitis, atopic dermatitis, Crohn's disease, Graves's disease, food
 CC allergies, allergic contact dermatitis, CLL cancers and/or B-cell
 CC lymphomas. They may also be used to treat a range of other diseases and
 CC disorders such as rheumatoid arthritis, ulcerative colitis, psoriasis,
 CC pigeon breeder's disease, hepatitis, leprosy, Lyme disease, diabetes
 CC mellitus, candidiasis and aplastic anaemia. They are also useful for
 CC inducing hyper-cross-linking of membrane antigens and for the
 CC preferential killing of selected cell populations.
 XX
 SQ Sequence 470 AA;

Query Match 90.9%; Score 2287; DB 21; Length 470;
 Best Local Similarity 91.1%; Pred. No. 7.5e-131;
 Matches 428; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 1 MCGWSCIIILFLVATATGVHSQVGVOLVSGAEVKPKGASVKVSCKASGYTFTSYNMOWVKQAP 60
 DB 1 MGSWIIILFLVATATVSLVSLVGLQPGAEIVKPGASVKMSCKASGYTFTSYNMHWKQCP 60

QY 61 GQGLEWGMGIDPSDGYTNYNQKFKGKATLTDVTSTAYMELSSLSRSEDYATVYCARNRD 120
 DB 61 grglewgaipngdtsynqkfkgkatltadksstaymqllsitsedsavyyccarsty 120

QY 121 YSNMYFDYWGEGTLVTVSSASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
 DB 121 Y9gdwyfnvwgagttvtvsaastckpsvflapsskstsggtaalgclvxdyfpvptvs 180
 QY 181 WNSGALTSVHTFPVAVLQSSGLYSLSVVTVTPSSSLGTQTYICNVNHPKSNNTKVDKRVPEP 240
 DB 181 wnsгалtsvhtcfpavlqssglyslssvvtpssslgtqtyicnvnhkpsntkvdkkvep 240
 QY 241 KSCDKTHTCCPPCAPPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVYVDSHEDPEVKFNW 300
 DB 241 kscdkthtccppcapellggpsvflfppkpkdtlmisrtpevtcvcvvdshedpevkfnw 300
 QY 301 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLDHDLWLNKGEYKCKVSNKALPAPIEKTIS 360
 DB 301 yvdgvevhnaktkpreeqynstyrvvsvltvldhdlwnkgeyckvsnkalpapiektis 360
 QY 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPV 420
 DB 361 kagqprepqvylppsrdeitknqvsltclykgfypsdiavewesngqpennnykttppv 420
 QY 421 LQSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
 DB 421 ldsdgsfflyskltvdksrwqgnvfscsvmhéalhnhytqkslsicpgk 470

RESULT 14
 AAE03755
 ID AAE03755 standard; Protein; 466 AA.
 XX
 AC AAE03755;
 XX
 DT 07-AUG-2001 (first entry)
 XX
 DE Chimeric 2403 IgG antibody heavy chain (5F2.4H4.1E3).
 XX
 KW Murine; prostate stem cell antigen; PSMA; cytostatic; gene therapy;
 KW glycoprotein; cancer; prostate; bladder; lung; tumour; Ab; antibody;
 KW human; immunoglobulin G; IgG; heavy chain region.
 XX
 OS Chimeric - Mus musculus.
 OS Chimeric - Homo sapiens.
 PH
 FT Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= Signal_peptide
 FT Protein 20..466
 FT /label= Mature_IgG_antibody_heavy_chain
 FT Region 1..141
 FT /note= "Derived from mouse heavy chain variable
 FT region (VH)"
 FT Region 142..466
 FT /note= "Derived from human IgG heavy chain constant
 FT region"
 XX
 PN WO200140309-A2.
 XX
 PD 07-JUN-2001.
 XX
 XX 27-OCT-2000; 2000WO-US29603.
 XX
 PR 29-OCT-1999; 99US-0162558.
 PR 16-FEB-2000; 2000US-0184872.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Devaux B, Keller G, Koeppe H, Lasky LA;
 XX
 DR WPI; 2001-389954/41.
 XX
 PT Novel anti-prostate stem cell antigen (PSMA) antibody that internalizes
 PT on binding to PSMA on mammalian cell and inhibits growth of
 PT PSMA-expressing cancer cells in vivo, useful for killing
 PT PSMA-expressing cancer cells -

xx PS Claim 5; Fig 13; 112pp; English.

xx CC The present chimeric sequence is full length 2403 immunoglobulin G (IgG)

xx CC antibody heavy chain (5F2.4H4.1E3) derived from murine heavy chain

xx CC variable region (VL) and human IgG heavy chain constant region.

xx CC This antibody binds to prostate stem cell antigen (PSCA) which is a

xx CC single subunit glycoprotein that is expressed on the cell surface as a

xx CC glycosylphosphatidylinositol (GPI)-anchored protein. The present

xx CC invention relates to anti-PSCA antibody composition and methods of

xx CC killing PSCA-expressing cancer cells. PSCA is useful for inhibiting and

xx CC killing the growth of PSCA-expressing cancer cells such as prostate

xx CC cancer, bladder cancer or lung cancer cells. Humanised antibody

xx CC conjugated to a toxin or a radioactive isotope is used for killing the

xx CC cancer cells. PSCA is useful for specifically targeting PSCA-expressing

xx CC tumour cells in vivo and for inhibiting or killing these cells. The

xx CC antibodies are also useful for treating the above mentioned cancers and

xx CC for diagnosing and staging of PSCA-expressing cancer, for purification

xx CC or immunoprecipitation of PSCA from cells, and for detection and

xx CC quantitation of PSCA in vitro. PSCA DNA is also useful for treating

xx CC cancers by gene therapy techniques.

xx SQ Sequence 466 AA;

Query Match 90.7%; Score 2283; DB 22; Length 466;

Best Local Similarity 91.1%; Pred. No. 1.3e-130;

Matches 428; Conservative 17; Mismatches 21; Indels 4; Gaps 1;

QY 1 MGWSCIIILFLVATATGHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVKQAP 60

DB 1 mgwsciiilflvatatgshsqvqlvqsgaevlkpgasvkvsckasgytftnylnwvkqr 60

QY 61 GQGLEWMEIDPDSYNYNOKFKGKATLTVDSTSTAYMELSLRSDTAVYICARNRD 120

DB 61 grglewmeidpsnyynokfkgtatltvdststaymelslsrdsdtaavyicartgi 120

QY 121 YSNWNYFDWGEGLTVTVSSASTGKPSVFLPAPSKSTSGGTAAALGCLVKDYFPEPVTVS 180

DB 121 ysnwnyfdwgeglvtvssastgkpsvflpapskstsggtaaalgcclvkdyfpepvtvs 176

QY 181 WNSGALTSGVHTFPVAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKRVPE 240

DB 177 wnsгалtsghvhtfpavlaqssglsylssvvtvpssslgtqtyicnvnhkpsntkvdckvpe 236

QY 241 KSCDKHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 300

DB 237 kscdkhtccpcpapelggpsvflfppkpkdtlmisrtpevtcvvdvshedpevkfnw 296

QY 301 YVDGVEVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIS 360

DB 297 yvdgvevhnatkpreeqynstyrvvsvltvlhqdwlngkeyckvsnkalpapiektis 356

QY 361 KAGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNKTTPPV 420

DB 357 kagqprepqvytlppsreemtknqvsltcclvkgfypsdiavewesngopennktppv 416

QY 421 LDSGSEFLYSLKLTVDKSRWQQGVFSCVNMHEALHNHYTQKSLSLSPGK 470

DB 417 ldsgsfflyslkltvdksrwqqgvfscvnmhealhnhytqkslsispgk 466

RESULT 15

AAB72232

ID AAB72232 standard; Protein; 464 AA.

xx AC AAB72232;

xx AC AAB72232;

xx DT 10-MAY-2001 (first entry)

xx DE Humanised 323/A3 (IgG1) antibody heavy chain amino acid sequence.

xx DE Anti-Ep-CAM antibody; cyclic adenosine monophosphate; cell synthesis;

KW chemotherapeutic agent; cytostatic; anti-cancer therapy; cancer;

KW heavy chain.

OS Mus sp.

OS Homo sapiens.

PN WO200107082-A1.

XX 01-FEB-2001.

XX 23-JUL-1999; 99WO-EP05271.

XX 23-JUL-1999; 99WO-EP05271.

XX (GLAX) GLAXO GROUP LTD.

XX Knick VC, Stimmel JB, Thurmond LM;

XX WPI; 2001-182729/18.

XX Combination for treating cancer (e.g. breast, gastric or prostate

PT cancers), or in the manufacture of a medicament for anti-cancer

PT therapy, comprises an anti-Ep-cyclic adenosine monophosphate antibody

PT with a chemotherapeutic agent -

XX Example 3; Fig 7; 103pp; English.

XX This invention relates to a combination of an anti-Ep-CAM (cyclic

CC adenosine monophosphate) antibody with a chemotherapeutic agent, that is

CC capable of arresting Ep-CAM antigen expressing cells in the synthesis (S)

CC phase or the second growth phase (M) of cell enlargement (G2)/DNA

CC replication. The antibody exhibits cytostatic activity and is useful in

CC the manufacture of a medicament for use in anti-cancer therapy.

CC characterised in that a chemotherapeutic agent, which is capable of

CC arresting Ep-CAM antigen expressing cells in S or in G2/M, is

CC co-administered to a patient with an anti-Ep-CAM antibody. The

CC combination is useful for treating cancer, particularly colorectal

CC cancer, breast cancer, gastric cancer, prostate cancer or non-small-cell

CC lung cancer. The present sequence represents the heavy chain of

CC anti-Ep-CAM antibody known as humanised 323/A3 (IgG1) which can be

CC used in the combination of the invention.

XX Sequence 464 AA;

Query Match 90.7%; Score 2282.5; DB 22; Length 464;

Best Local Similarity 91.7%; Pred. No. 1.4e-130;

Matches 430; Conservative 14; Mismatches 20; Indels 5; Gaps 2;

QY 1 MGWSCIIILFLVATATGHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVKQAP 60

DB 1 mgwsciiilflvatatgshsqvqlvqsgaevlkpgasvkvsckasgytftnygmwvrqap 60

QY 61 GQGLEWMEIDPDSYNYNOKFKGKATLTVDSTSTAYMELSLRSDTAVYICARNRD 120

DB 61 gqglewmeidpsnyynokfkgtatltvdststaymelslsrdsdtaavyicarnd 117

QY 121 YSNWNYFDWGEGLTVTVSSASTGKPSVFLPAPSKSTSGGTAAALGCLVKDYFPEPVTVS 180

DB 118 ysnwnyfdwgeglvtvssastgkpsvflpapskstsggtaaalgcclvkdyfpepvtvs 175

QY 181 WNSGALTSGVHTFPVAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKRVPE 240

DB 176 wnsгалtsghvhtfpavlaqssglsylssvvtvpssslgtqtyicnvnhkpsntkvdckvpe 235

QY 241 KSCDKHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 300

DB 236 kscdkhtccpcpapelggpsvflfppkpkdtlmisrtpevtcvvdvshedpevkfnw 295

QY 301 YVDGVEVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIS 360

DB 296 yvdgvevhnatkpreeqynstyrvvsvltvlhqdwlngkeyckvsnkalpapiektis 355

QY 361 KAKGPREPOVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVWESNGOPENNYKTTTPV 420
Db |||||
QY 356 kakgprepqvylppsrdeitknqvsitcivkgfypsdiawesngqpennykttppv 415
Db |||||
QY 421 LDSGSEFLYKLTVDKSRWQQGNVFCGVMHEALHNHYTQKSLSLSPG 469
Db |||||
QY 416 ldsdgsfflyskltvdksrwqgnvfscvmhealhnhytqkslsispg 464
Db |||||

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Job time: 148 sec

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OM protein - protein search, using sw model

Run on: April 17, 2002, 16:39:21 ; Search time 21.24 Seconds

(without alignments)
497.954 Million cell updates/sec

Title: US-09-499-662-117
Perfect score: 2517
Sequence: 1 MWSCILFLVATATGVHSQ.....MHEALHNHYTQKSLSPGK 470

Scoring table: BLOSOM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2229	88.6	449	1	US-08-458-516-13
2	2227	88.5	476	2	Sequence 13, Appl
3	2199.5	87.4	467	4	US-08-378-939-10
4	2197.5	87.3	452	3	US-09-049-672A-8
5	2197.5	87.3	452	3	US-09-027-449-71
6	2161.5	85.9	454	2	US-09-026-985-71
7	2161.5	85.9	454	2	US-07-934-373C-22
8	2161.5	85.9	454	5	PCT-US93-07832-22
9	2121	84.3	451	2	US-08-887-352B-14
10	2121	84.3	451	2	US-08-887-352B-16
11	2121	84.3	451	3	US-08-466-151-65
12	2121	84.3	451	4	US-09-109-207C-14
13	2121	84.3	451	4	US-09-109-207C-16
14	2121	84.3	451	4	US-09-296-005-16
15	2121	84.3	451	4	US-09-296-005-16
16	2118	84.1	478	3	US-08-487-550-8
17	2113	83.9	451	2	US-08-887-352B-18
18	2113	83.9	451	4	US-09-109-207C-18
19	2113	83.9	451	4	US-09-282-505-2
20	2113	83.9	451	4	US-09-054-255-2
21	2113	83.9	451	4	US-09-296-005-18
22	2102	83.5	453	3	US-08-466-151-8
23	2100.5	83.5	467	2	US-07-916-098A-45
24	2096.5	83.3	552	5	PCT-US93-07832-23
25	2093.5	83.2	469	2	US-07-934-373C-23
26	2093.5	83.2	469	3	US-08-437-642B-23
27	2087.5	82.9	459	1	US-08-157-101A-7

28 2069.5 82.2 467 1 US-08-704-744-81 Sequence 81, Appl
29 2067.5 82.1 473 4 US-09-049-672A-4 Sequence 4, Appl
30 2060.5 81.9 445 4 US-08-341-560B-17 Sequence 17, Appl
31 2054 81.6 476 3 US-08-487-550-12 Sequence 12, Appl
32 2051.5 81.5 446 3 US-08-397-411-7 Sequence 7, Appl
33 2022 80.3 476 3 US-08-487-550-4 Sequence 4, Appl
34 2019 80.2 442 5 PCT-US96-10043-9 Sequence 9, Appl
35 2007 79.7 442 1 US-08-461-968A-5 Sequence 5, Appl
36 2007 79.7 442 2 US-08-462-571-5 Sequence 5, Appl
37 1992.5 79.2 450 2 US-08-788-800-12 Sequence 12, Appl
38 1983 78.8 442 1 US-08-480-036-2 Sequence 2, Appl
39 1983 78.8 442 1 US-08-461-968A-2 Sequence 2, Appl
40 1983 78.8 442 2 US-08-462-571-2 Sequence 2, Appl
41 1983 78.8 442 5 PCT-US96-10043-12 Sequence 12, Appl
42 1945 77.3 443 5 PCT-US96-13152-4 Sequence 4, Appl
43 1875.5 74.5 467 4 US-08-523-894-8 Sequence 12, Appl
44 1874.5 74.5 467 4 US-08-523-894-8 Sequence 8, Appl
45 1867.5 74.2 467 4 US-08-523-894-10 Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-458-516-13
; Sequence 13, Application US/08458516
; Patent No. 5777085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 449 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-458-516-13

Query Match 88.6%; Score 2229; DB 1; Length 449;
Best Local Similarity 92.9%; Pred. No. 8.4e-160;
Matches 419; Conservative 15; Mismatches 15; Indels 2; Gaps 2;

QY 20 QVQLVQSGAEVKKPKASVKVSKASGYTFTSYWQWVKQAPQGQLEWNGEIDPDSSTNY 79
Db 1 QVQLVQSGAEVKKPKGSSVKVSKASGYFTSYLIEWRQAPQGQLEWIGVYPGSGGTNY 60
QY 80 NQKFKGKATLVDTSTAYMELSSLSRSEDPAVYVCARNRDYSNNWYFDVWGEGLTVTS 139
Db 61 NEKFKGRVTLVDSTWYAYMELSSLSRSEDPAVYFCAR-RDNGYCW-FAYWQGTFLTVTS 118
QY 140 SASTKGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPVTVVSWNSGALTSGVHTTTPAVLQS 199
Db 119 SASTKGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPVTVVSWNSGALTSGVHTTTPAVLQS 178
QY 200 SGLYSLSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKRVKPSCKDTHCPCPAPELLG 259
Db 179 SGLYSLSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKRVKPSCKDTHCPCPAPELLG 238
QY 260 GPSVFLPAPKPKDLMISRTPEVTVVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQY 319
Db 239 GPSVFLPAPKPKDLMISRTPEVTVVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQY 298
QY 320 NSTYRVVSVTLVHLDWLNKGYCKVCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRE 379
Db 299 NSTYRVVSVTLVHLDWLNKGYCKVCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRE 358
QY 380 EMTKNQVSLCLVKGFYPSDIAVWESNGPENNYKTPPVLDSDGSEFFLYSKLTVDKSR 439
Db 359 ELTRNQVSLCLVKGFYPSDIAVWESNGPENNYKTPPVLDSDGSEFFLYSKLTVDKSR 418
QY 440 WQGNVFCSCVMHEALHNHYTKLSLSPGK 470
Db 419 WQGNVFCSCVMHEALHNHYTKLSLSPGK 449

RESULT 2

US-08-378-939-10
; Sequence 10, Application US/08378939
; Patent No. 5876961
; GENERAL INFORMATION:
; APPLICANT: CROME, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
; STREET: 555 THIRTEENTH ST. N.W.
; CITY: WASHINGTON
; STATE: D. C.
; COUNTRY: U.S.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,939
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/952640
; FILING DATE: 01-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, BARBARA G
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1808-118
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: protein
US-08-378-939-10

Query Match 88.5%; Score 2227; DB 2; Length 476;
Best Local Similarity 88.2%; Pred. No. 1.3e-159;
Matches 420; Conservative 22; Mismatches 28; Indels 6; Gaps 1;

QY 1 MGWSCIIILFLVATATGVHSGVQLVQSGAEVKKPKASVKVSKASGYTFTSYWQWVKQAP 60
Db 1 MDWTRELFVVAATGVQSQGVQVQSGAEVKKPKGSSVTVVSKASGGTFSNVAISWVRQAP 60
QY 61 GQGLEWNGEIDPDSSTNYNOKFKGKATLVDTSTAYMELSSLSRSEDPAVYVCARNR- 119
Db 61 GQGLEWNGEIIPLFGTPTYSQNFQGRVTITADKSTSTAHMELTSLRSEDPAVYICATDRY 120
QY 120 -----DYSNNWYFDVWGEGLTVVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFP 174
Db 121 RQANFDRARVGVFPWQGTTLTVVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFP 180
QY 175 EPVTVVSWNSGALTSGVHTTTPAVLOSGLYSLSSVTVVPSLSLGTQTYICNVNHNKPSNTKV 234
Db 181 EPVTVVSWNSGALTSGVHTTTPAVLOSGLYSLSSVTVVPSLSLGTQTYICNVNHNKPSNTKV 240
QY 235 DKRVEPKSCDKTHRCPCPAPELLGGPSVFLFPPPKDTHLMSRTPEVTVVVDVSHEDP 294
Db 241 DKRVEPKSCDKTHRCPCPAPELLGGPSVFLFPPPKDTHLMSRTPEVTVVVDVSHEDP 300
QY 295 EVKFNWYDGVGVHNAKTKPREEQYNSTYRVVSVTLVHLDWLNKGYCKVCKVSNKALPAP 354
Db 301 EVKFNWYDGVGVHNAKTKPREEQYNSTYRVVSVTLVHLDWLNKGYCKVCKVSNKALPAP 360
QY 355 IEKTIKAKGQPREPOVYITLPPSREEMTKNOVSLTCLVKGFYPSDIAVWESNGPENNY 414
Db 361 IEKTIKAKGQPREPOVYITLPPSRDELTKNOVSLTCLVKGFYPSDIAVWESNGPENNY 420
QY 415 KTTPLVLDSDGSEFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKLSLSPGK 470
Db 421 KTTPLVLDSDGSEFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKLSLSPGK 476

RESULT 3

US-09-049-672A-8
; Sequence 8, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,672A
; FILING DATE: HEREWITH
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0497 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGUT11
; CLONE: 2747531
; US-09-049-672A-8

Query Match      87.4%; Score 2199.5; DB 4; Length 467;
Best Local Similarity 89.0%; Pred. No. 1.5e-157;
Matches 413; Conservative 20; Mismatches 28; Indels 3; Gaps 1;

QY 7 ILFLVATGTHSVQVLSGAEVKKPGASVKVSKASGYTFTSYMMQWVKQAPGGLEW 66
Db 7 ILFLVAAATGTHSVQVLSGAEVKKPGASVQVCTVSGFTLSDLSVHWVROAPGGLEW 66
QY 67 MGEIDPSDSTNNYKFKGKATLTVDTSSTAYMELSLRSEDATVYICARNRDYSNNWY 126
Db 67 MGLPAPNGEAVYAKFLGRULFSLSEDTSADTAIMEFLNNIGSEDSAIYYCARQH---YDFP 123
QY 127 PDVWGEGTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSVNSGAL 186
Db 124 PDEWQGTMTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSVNSGAL 183
QY 187 TSGVHTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKT 246
Db 184 TSGVHTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKT 243
QY 247 HTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVE 306
Db 244 HTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVE 303
QY 307 VHNAKTKPREEQNSTYRVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKAKGQP 366
Db 304 VHNAKTKPREEQNSTYRVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKAKGQP 363
QY 367 REPQVYTLPPSREEMTKNOVSLTCLVKGYFSDIAVEWESNQGPENNYKTTTPVLDSDGS 426
Db 364 REPQVYTLPPSREEMTKNOVSLTCLVKGYFSDIAVEWESNQGPENNYKTTTPVLDSDGS 423
QY 427 FELYSKLTVDKSRWQGVNFCVSMVHEALHNNHYTKLSLSPGK 470
Db 424 FELYSKLTVDKSRWQGVNFCVSMVHEALHNNHYTKLSLSPGK 467

RESULT 4
US-09-027-449-71
; Sequence 71, Application US/09027449
; Patent No. 6025158
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
```

```
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/027,449
; FILING DATE: 20-Feb-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/074,330
; FILING DATE: 22-Jan-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/038,664
; FILING DATE: 21-Feb-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R3-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-027-449-71

Query Match      87.3%; Score 2197.5; DB 3; Length 452;
Best Local Similarity 89.8%; Pred. No. 2e-157;
Matches 406; Conservative 28; Mismatches 17; Indels 1; Gaps 1;

QY 20 QVOLVOSGAEVKKPGASVKVSKASGYTFTSYMMQWVKQAPGGLEMMGIDPSDSTNY 79
Db 1 EVQLVQSGGGLVPGGSLRLSCAASGSFSSHYMHVVRQAPGKGLWGVYIDPSNGETTY 60
QY 80 NQKFKGKATLTVDTSSTAYMELSLRSEDATVYICARNRDYSNNWYFDVWGEGTLTV 138
Db 61 NQKFKGRFTLSRDNSKNTAYLQHNLSRAEDTAVYICARGDYRNGDMFFDVGQGLTV 120
QY 139 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSVNSGALTSVHTFFAVLQ 198
Db 121 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSVNSGALTSVHTFFAVLQ 180
QY 199 SSGLSLSSVTVPPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPEL 258
Db 181 SSGLSLSSVTVPPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPEL 240
QY 259 GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQ 318
Db 241 GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQ 300
QY 319 YNSTYRVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378
Db 301 YNSTYRVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 360
QY 379 EEMTKNOVSLTCLVKGYFSDIAVEWESNQGPENNYKTTTPVLDSDGSFELYSKLTVDKS 438
Db 361 EEMTKNOVSLTCLVKGYFSDIAVEWESNQGPENNYKTTTPVLDSDGSFELYSKLTVDKS 420
QY 439 RWOQGVNFCVSMVHEALHNNHYTKLSLSPGK 470
Db 421 RWOQGVNFCVSMVHEALHNNHYTKLSLSPGK 452

RESULT 5
US-09-026-985-71
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QY 317 EOYNSTYRVSVTLVHODWLNKKEYCKVSNKALPAPIEKTISKAKGPREPQVYTLPP 376
DB 301 EOYNSTYRVSVTLVHODWLNKKEYCKVSNKALPAPIEKTISKAKGPREPQVYTLPP 360
QY 377 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNKTTPPVLDSDGSFFLYSKLTV 436
DB 361 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNKTTPPVLDSDGSFFLYSKLTV 420
QY 437 KSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470
DB 421 KSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 454

RESULT 7
US-08-437-642B-22
; Sequence 22, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 454 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-437-642B-22

Query Match 85.9%; Score 2161.5; DB 3; Length 454;
Best Local Similarity 89.4%; Pred. No. 1e-154;
Matches 406; Conservative 17; Mismatches 28; Indels 3; Gaps 1;

QY 20 QVOLVQSGAEVKKPGASVKVSCKGQVFTTYSWMQVWKVQAPQGLWMEIDPDSYTN 79
DB 1 QVOLVQSGAEVKKPGASVKVSCKGQVFTTYSWMQVWKVQAPQGLWMEIDPDSYTN 60

QY 80 NQKFKGKATLTVDTSSTAYMELSLRSEDYAVYYCARNRDYSNNW---YFDWMGEGTLY 136
DB 61 NQRFMDKATLAVDKSTSTAYMELSLRSEDYAVYYCARNRGLNYGDFRYFDWMGAGTTV 120
QY 137 TVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 196
DB 121 TVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 180
QY 197 LQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHCTCPCPAPE 256
DB 181 LQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHCTCPCPAPE 240
QY 257 LLGGPSVFLFPPKPKDRLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 316
DB 241 LLGGPSVFLFPPKPKDRLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 300
QY 317 EOYNSTYRVSVTLVHODWLNKKEYCKVSNKALPAPIEKTISKAKGPREPQVYTLPP 376
DB 301 EOYNSTYRVSVTLVHODWLNKKEYCKVSNKALPAPIEKTISKAKGPREPQVYTLPP 360
QY 377 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNKTTPPVLDSDGSFFLYSKLTV 436
DB 361 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNKTTPPVLDSDGSFFLYSKLTV 420
QY 437 KSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470
DB 421 KSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 454

RESULT 8
PCT-US93-07832-22
; Sequence 22, Application PC/TUS9307832
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Immunglobulin Variants
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07832
; FILING DATE: 19930820
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 709P2PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX: 415/952-9881
; TELEEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 454 amino acids


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; REGISTRATION NUMBER: 39, 044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-887-352B-16

Query Match      84.3%; Score 2121; DB 2; Length 451;
Best Local Similarity 87.4%; Prod. No. 1.1e-151;
Matches 395; Conservative 25; Mismatches 30; Indels 2; Gaps 2;

QY 20 QVQLVQSGAEVKKPGASVKYCKSKAGSYFTFS-YMMQVVKQAPGGQLEWGMGIDPSDSYTN 78
DB 1 EVQLVESGGGLVQPGGSLRLISCAVGSYISITSGYSWNIQAPGKGLWEWASI-TYDGSNTN 59

QY 79 YNOKFKKATLTVDTSITSTAYMELSSLRSEDTAVYYCARNRDYNNWYFDVWVGEGTLTV 138
DB 60 YNPSVKGRITISRDDSKNTFYLMNLSRAEDTAVYYCARGSHYGHWHFAVWGQGLTV 119

QY 139 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQ 198
DB 120 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQ 179

QY 199 SSGLYSLSSVTVYVSSSLGQTTCYCNVNHKPSNTKVDKRVPEKSCDKTHTCPPCPAPELL 258
DB 180 SSGLYSLSSVTVYVSSSLGQTTCYCNVNHKPSNTKVDKRVPEKSCDKTHTCPPCPAPELL 239

QY 259 GGPSVFLEPPKPKDTLMISRTPEVTCVVDVSHEDPEVKENWYDGVGVHNAKTKPREEQ 318
DB 240 GGPSVFLEPPKPKDTLMISRTPEVTCVVDVSHEDPEVKENWYDGVGVHNAKTKPREEQ 299

QY 319 YNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPVYTLPPSR 378
DB 300 YNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPVYTLPPSR 359

QY 379 EEMTKNQVSLTCLVKGYFSPDSIAEWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVDKS 438
DB 360 EEMTKNQVSLTCLVKGYFSPDSIAEWESNGOPENNYKTTTPVLDSDGSFFLYSKLTVDKS 419

QY 439 RWQGNVFCFSVMHEALHNHYTQKSLSLSPGK 470
DB 420 RWQGNVFCFSVMHEALHNHYTQKSLSLSPGK 451

RESULT 11
US-08-466-151-65
; Sequence 65, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardiue, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151

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[illegible]

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Db 1 EVQLVESGGGLVQPGGSLRLSCAVGSYITSGYSNHWIRQAPGKGLEWVASI-TYDGSIN 59
QY 79 YNQKFKGKATLVDTSTAYMELSLRSEDVAVYICARNRDYNNWYFDVWGEGTLTV 138
Db 60 YNPSVKGRITISRDOSKNTFYIQLMNSLRAEDTAVYICARGSHYFGHWFAVWGQGTFLTV 119
QY 139 SSASTKGPSVFFLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTTTPAVLIQ 198
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QY 199 SSGLYSLSSVVTVPSSSLGTQYIICNVNHPKNTKVDKRVKPKSCDKTHTCPCPAPELL 258
Db 180 SSGLYSLSSVVTVPSSSLGTQYIICNVNHPKNTKVDKRVKPKSCDKTHTCPCPAPELL 239
QY 259 GGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNNAKTKPREEQ 318
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QY 319 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSR 378
Db 300 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSR 359
QY 379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELYSKLTVDKS 438
Db 360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELYSKLTVDKS 419
QY 439 RWOQGNVFSCSVNHEALHNHYTQKSLSLSPGK 470
Db 420 RWOQGNVFSCSVNHEALHNHYTQKSLSLSPGK 451
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RESULT 15

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US-09-296-005-16
; Sequence 16, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-Ige Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123C1r
; CURRENT APPLICATION NUMBER: US/09/296,005
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/887,352
; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 16
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAEL1
US-09-296-005-16
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Query Match 84.3%; Score 2121; DB 4; Length 451;
Best Local Similarity 87.4%; Pred. NO. 1.1e-151;
Matches 395; Conservative 25; Mismatches 30; Indels 2; Gaps 2;

QY 20 QVQLVQSGAEVKKPGASVKVSCKASQGYTFTS-YHWQWVKQAPGQGLEWMGEIDPSDSYTN 78
Db 1 EVQLVESGGGLVQPGGSLRLSCAVGSYITSGYSNHWIRQAPGKGLEWVASI-TYDGSIN 59

QY 79 YNQKFKGKATLVDTSTAYMELSLRSEDVAVYICARNRDYNNWYFDVWGEGTLTV 138
Db 60 YNPSVKGRITISRDOSKNTFYIQLMNSLRAEDTAVYICARGSHYFGHWFAVWGQGTFLTV 119

QY 139 SSASTKGPSVFFLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTTTPAVLIQ 198
Db 120 SSASTKGPSVFFLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTTTPAVLIQ 179

QY 199 SSGLYSLSSVVTVPSSSLGTQYIICNVNHPKNTKVDKRVKPKSCDKTHTCPCPAPELL 258
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Db 180 SSGLYSLSSVVTVPSSSLGTQYIICNVNHPKNTKVDKRVKPKSCDKTHTCPCPAPELL 239
QY 259 GGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNNAKTKPREEQ 318
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QY 319 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSR 378
Db 300 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSR 359
QY 379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELYSKLTVDKS 438
Db 360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELYSKLTVDKS 419
QY 439 RWOQGNVFSCSVNHEALHNHYTQKSLSLSPGK 470
Db 420 RWOQGNVFSCSVNHEALHNHYTQKSLSLSPGK 451
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Search completed: April 17, 2002, 16:39:22
Job time: 145 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 17, 2002, 16:39:53 ; Search time 25.85 Seconds
(without alignments)
1384.992 Million cell updates/sec

Title: US-09-499-662-117
Perfect score: 2517
Sequence: 1 MWSCILFLVAFATGVHSQ.....MHEALNHVYTKLSLSPOK 470

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR-68.*

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1758	69.8	330	1 GHU	Ig gamma-1 chain C
2	1639.5	65.1	377	2 A23511	Ig gamma-3 chain C
3	1637.5	65.1	377	2 A60764	Ig gamma-3 chain C
4	1610.5	64.0	469	2 S37483	Ig gamma-2a chain
5	1610	64.0	326	1 G2HU	Ig gamma-2 chain C
6	1599.5	63.5	327	1 G4HU	Ig gamma-4 chain C
7	1546	61.4	474	1 G2MS11	Ig gamma-2b chain
8	1544	61.3	446	2 S40295	Ig gamma-2a chain
9	1501.5	59.7	475	2 S01321	Ig gamma-2b chain
10	1471	58.4	470	2 S22080	Ig heavy chain pre
11	1467	58.3	472	2 S31459	Ig gamma-1 chain -
12	1432.5	56.9	444	2 PC4436	monoclonal antibod
13	1429	56.8	374	2 S69339	Ig heavy chain V r
14	1267	50.3	328	2 I47159	Ig gamma 2a chain
15	1261	50.1	328	2 I47160	Ig gamma 2b chain
16	1253	49.8	255	4 S31866	Ig gamma-1 chain C
17	1245	49.5	234	2 PT0207	Ig gamma chain C r
18	1235	49.1	328	2 I47158	Ig gamma 1 chain C
19	1231.5	48.9	323	1 GHRB	Ig gamma chain C r
20	1231	48.9	328	2 I47161	Ig gamma 3 chain C
21	1210.5	48.1	329	1 G2GP	Ig gamma-2 chain C
22	1165.5	46.3	308	2 C30554	Ig heavy chain C r
23	1157	46.0	289	1 G3HUW1	Ig gamma-3 heavy C
24	1155	45.9	326	2 PS0017	Ig gamma-1 chain C
25	1150	45.7	329	1 G3MSC	Ig gamma-3 chain C
26	1145	45.5	324	1 G1MS	Ig gamma-1 chain C
27	1144.5	45.5	333	2 PS0018	Ig gamma-2b chain
28	1140	45.3	393	1 G1MSM	Ig gamma-1 chain C
29	1139	45.3	398	1 G3MSM	Ig gamma-3 chain C

Ig gamma-2a chain
Ig gamma-2c chain
Ig gamma-2a chain
Ig gamma-2a chain
Ig gamma-2a chain
Ig gamma-2a chain
Ig gamma-2b chain C
Ig gamma-2b chain
Ig gamma 4 chain C
Ig epsilon chain C
Ig mu chain precu
Ig heavy chain C
Ig heavy chain (DO
Ig gamma chain - m
Ig gamma-1 heavy c
Ig heavy chain VHI
Ig Y heavy chain (

ALIGNMENTS

RESULT 1
GHU
Ig gamma-1 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999
C:Accession: A93433; S3887; B90563; A90564; B91668; A91723; A02146
R:Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A:Reference number: A93433; MUID:82274238
A:Accession: A93433
A:Molecule type: DNA
A:Residues: 1-330 <ELL>
A:Cross-references: EMBL:Z17370
A:Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) marker
A:Note: Lys-330 is removed after translation
R:Harris, L.J.
submitted to the EMBL Data Library, October 1992
A:Reference number: S33904
A:Accession: S36861
A:Molecule type: DNA
A:Residues: 2-330 <HAR>
A:Cross-references: EMBL:Z17370
R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of
A:Reference number: S33887; MUID:83001943
A:Accession: S33887
A:Molecule type: DNA
A:Residues: 88-113;235-330 <TAK>
A:Cross-references: EMBL:Z17370
R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman
Biochemistry 9, 3161-3170, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seq
A:Reference number: A90563; MUID:71064024
A:Contents: myeloma protein Eu
A:Accession: B90563
A:Molecule type: protein
A:Residues: 1-96,'R',98-135 <CUN>
A:Note: this sequence has the G1m(3) marker, 97-Arg
R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se
A:Reference number: A90564; MUID:71064025
A:Contents: Eu
A:Accession: A90564
A:Molecule type: protein
A:Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',2
A:Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met
R:Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A:Title: Die Primerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Ni

Igen Primaerstruktur.
A:Reference number: A91668; MUID:77070269
A:Contents: myeloma protein Nie
A:Accession: B91668
A:Molecule type: protein
A:Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',270-300,'L',302-318,'D',320-330,'L',332-348,'E',350-366,'K',368-384,'D',386-402,'L',404-420,'E',422-438,'D',440-456,'L',458-474,'E',476-492,'L',494-510,'E',512-528,'D',530-546,'L',548-564,'E',566-582,'D',584-600,'L',602-618,'E',620-636,'D',638-654,'L',656-672,'E',674-690,'L',692-708,'E',710-726,'D',728-744,'L',746-762,'E',764-780,'D',782-798,'L',800-816,'E',818-834,'D',836-852,'L',854-870,'E',872-888,'D',890-906,'L',908-924,'E',926-942,'D',944-960,'L',962-978,'E',980-996,'D',998-1014,'L',1016-1032,'E',1034-1050,'D',1052-1068,'L',1070-1086,'E',1088-1104,'D',1106-1122,'L',1124-1140,'E',1142-1158,'D',1160-1176,'L',1178-1194,'E',1196-1212,'D',1214-1230,'L',1232-1248,'E',1250-1266,'D',1268-1284,'L',1286-1302,'E',1304-1320,'D',1322-1338,'L',1340-1356,'E',1358-1374,'D',1376-1392,'L',1394-1410,'E',1412-1428,'D',1430-1446,'L',1448-1464,'E',1466-1482,'D',1484-1500,'L',1502-1518,'E',1520-1536,'D',1538-1554,'L',1556-1572,'E',1574-1590,'D',1592-1608,'L',1610-1626,'E',1628-1644,'D',1646-1662,'L',1664-1680,'E',1682-1698,'D',1700-1716,'L',1718-1734,'E',1736-1752,'D',1754-1770,'L',1772-1788,'E',1790-1806,'D',1808-1824,'L',1826-1842,'E',1844-1860,'D',1862-1878,'L',1880-1896,'E',1898-1914,'D',1916-1932,'L',1934-1950,'E',1952-1968,'D',1970-1986,'L',1988-2004,'E',2006-2022,'D',2024-2040,'L',2042-2058,'E',2060-2076,'D',2078-2094,'L',2096-2112,'E',2114-2130,'D',2132-2148,'L',2150-2166,'E',2168-2184,'D',2186-2202,'L',2204-2220,'E',2222-2238,'D',2240-2256,'L',2258-2274,'E',2276-2292,'D',2294-2310,'L',2312-2328,'E',2330-2346,'D',2348-2364,'L',2366-2382,'E',2384-2400,'D',2402-2418,'L',2420-2436,'E',2438-2454,'D',2456-2472,'L',2474-2490,'E',2492-2508,'D',2510-2526,'L',2528-2544,'E',2546-2562,'D',2564-2580,'L',2582-2598,'E',2600-2616,'D',2618-2634,'L',2636-2652,'E',2654-2670,'D',2672-2688,'L',2690-2706,'E',2708-2724,'D',2726-2742,'L',2744-2760,'E',2762-2778,'D',2780-2796,'L',2798-2814,'E',2816-2832,'D',2834-2850,'L',2852-2868,'E',2870-2886,'D',2888-2904,'L',2906-2922,'E',2924-2940,'D',2942-2958,'L',2960-2976,'E',2978-2994,'D',2996-3012,'L',3014-3030,'E',3032-3048,'D',3050-3066,'L',3068-3084,'E',3086-3102,'D',3104-3120,'L',3122-3138,'E',3140-3156,'D',3158-3174,'L',3176-3192,'E',3194-3210,'D',3212-3228,'L',3230-3246,'E',3248-3264,'D',3266-3282,'L',3284-3300,'E',3302-3318,'D',3320-3336,'L',3338-3354,'E',3356-3372,'D',3374-3390,'L',3392-3408,'E',3410-3426,'D',3428-3444,'L',3446-3462,'E',3464-3480,'D',3482-3498,'L',3500-3516,'E',3518-3534,'D',3536-3552,'L',3554-3570,'E',3572-3588,'D',3590-3606,'L',3608-3624,'E',3626-3642,'D',3644-3660,'L',3662-3678,'E',3680-3696,'D',3698-3714,'L',3716-3732,'E',3734-3750,'D',3752-3768,'L',3770-3786,'E',3788-3804,'D',3806-3822,'L',3824-3840,'E',3842-3858,'D',3860-3876,'L',3878-3894,'E',3896-3912,'D',3914-3930,'L',3932-3948,'E',3950-3966,'D',3968-3984,'L',3986-4002,'E',4004-4020,'D',4022-4038,'L',4040-4056,'E',4058-4074,'D',4076-4092,'L',4094-4110,'E',4112-4128,'D',4130-4146,'L',4148-4164,'E',4166-4182,'D',4184-4200,'L',4202-4218,'E',4220-4236,'D',4238-4254,'L',4256-4272,'E',4274-4290,'D',4292-4308,'L',4310-4326,'E',4328-4344,'D',4346-4362,'L',4364-4380,'E',4382-4398,'D',4400-4416,'L',4418-4434,'E',4436-4452,'D',4454-4470,'L',4472-4488,'E',4490-4506,'D',4508-4524,'L',4526-4542,'E',4544-4560,'D',4562-4578,'L',4580-4596,'E',4598-4614,'D',4616-4632,'L',4634-4650,'E',4652-4668,'D',4670-4686,'L',4688-4704,'E',4706-4722,'D',4724-4740,'L',4742-4758,'E',4760-4776,'D',4778-4794,'L',4796-4812,'E',4814-4830,'D',4832-4848,'L',4850-4866,'E',4868-4884,'D',4886-4902,'L',4904-4920,'E',4922-4938,'D',4940-4956,'L',4958-4974,'E',4976-4992,'D',4994-5010,'L',5012-5028,'E',5030-5046,'D',5048-5064,'L',5066-5082,'E',5084-5100,'D',5102-5118,'L',5120-5136,'E',5138-5154,'D',5156-5172,'L',5174-5190,'E',5192-5208,'D',5210-5226,'L',5228-5244,'E',5246-5262,'D',5264-5280,'L',5282-5298,'E',5300-5316,'D',5318-5334,'L',5336-5352,'E',5354-5370,'D',5372-5388,'L',5390-5406,'E',5408-5424,'D',5426-5442,'L',5444-5460,'E',5462-5478,'D',5480-5496,'L',5498-5514,'E',5516-5532,'D',5534-5550,'L',5552-5568,'E',5570-5586,'D',5588-5604,'L',5606-5622,'E',5624-5640,'D',5642-5658,'L',5660-5676,'E',5678-5694,'D',5696-5712,'L',5714-5730,'E',5732-5748,'D',5750-5766,'L',5768-5784,'E',5786-5802,'D',5804-5820,'L',5822-5838,'E',5840-5856,'D',5858-5874,'L',5876-5892,'E',5894-5910,'D',5912-5928,'L',5930-5946,'E',5948-5964,'D',5966-5982,'L',5984-6000,'E',6002-6018,'D',6020-6036,'L',6038-6054,'E',6056-6072,'D',6074-6090,'L',6092-6108,'E',6110-6126,'D',6128-6144,'L',6146-6162,'E',6164-6180,'D',6182-6198,'L',6200-6216,'E',6218-6234,'D',6236-6252,'L',6254-6270,'E',6272-6288,'D',6290-6306,'L',6308-6324,'E',6326-6342,'D',6344-6360,'L',6362-6378,'E',6380-6396,'D',6398-6414,'L',6416-6432,'E',6434-6450,'D',6452-6468,'L',6470-6486,'E',6488-6504,'D',6506-6522,'L',6524-6540,'E',6542-6558,'D',6560-6576,'L',6578-6594,'E',6596-6612,'D',6614-6630,'L',6632-6648,'E',6650-6666,'D',6668-6684,'L',6686-6702,'E',6704-6720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Nature 221, 145-148, 1969
 A:Title: Structural studies of immunoglobulin G.
 A:Reference number: A93157; MUID:69064124

A:Contents: annotation; Sa, disulfide bonds
 C:Genetics:

A:Gene: GDB:IGHG2

A:Cross-references: GDB:119338; OMIM:147110
 A:Map position: 14q32.33-14q32.33

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (lambda) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger aggregates.

C:Superfamily: Immunoglobulin C region; immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:133-202/Domain: immunoglobulin homology <IM1>

F:134-203/Domain: immunoglobulin homology <IM2>

F:239-306/Domain: immunoglobulin homology <IM3>

F:14/Disulfide bonds: Interchain (to light chain) #status experimental

F:27-83,140-200,246-304/Disulfide bonds: #status experimental

F:102,103,106,109/Disulfide bonds: Interchain (to heavy chain) #status experimental

F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 64.0%; Score 1610; DB 1; Length 326;

Best Local Similarity 91.8%; Pred. No. 1e-84;

Matches 303; Conservative 10; Mismatches 13; Indels 4; Gaps 2;

QY 141 ASTKGPSVFPLAPSSKSTSGTAAALCLVDPPEPVTWNSGALTSGVHTFPAVLQSS 200

Db 1 ASTKGPSVFPLAPSSKSTSGTAAALCLVDPPEPVTWNSGALTSGVHTFPAVLQSS 60

QY 201 GLYSLSSVTVVPSSSLGTQTYICNVNHPKSNKVDKRVKPKSCDKTHTCPPCAPELLGG 260

Db 61 GLYSLSSVTVVPSSSLGTQTYICNVNHPKSNKVDKRVKPKSCDKTHTCPPCAPELLGG 260

QY 261 PSVFLPPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNKATKPREQYN 320

Db 117 PSVFLPPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNKATKPREQYN 320

QY 321 STYRVSVLVTLVHODWLNKEYCKVSNKALPAPIETKISKAKGQPREPOVYTLPPSREE 380

Db 177 STYRVSVLVTLVHODWLNKEYCKVSNKALPAPIETKISKAKGQPREPOVYTLPPSREE 380

QY 381 MTKNQVSLTCLVGFPSDIAVWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 440

Db 237 MTKNQVSLTCLVGFPSDIAVWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 440

QY 441 QQGNVFCSCVHHEALHNHYTQKSLSLSPGK 470

Db 297 QQGNVFCSCVHHEALHNHYTQKSLSLSPGK 326

RESULT 6

G4HU

Ig gamma-4 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999

C:Accession: A90933; A90249; A02150

R:Ellison, J.; Buxbaum, J.; Hood, L.

A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

A:Reference number: A90933; MUID:83157104

A:Accession: A90933

A:Molecule type: DNA

A:Residues: 1-327 <ELL>

A:Note: the sequence was determined from the germline gene

R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.

Biochem. J. 117, 33-47, 1970

A:Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant region of the heavy chain of human IgG1.

A:Reference number: A90249; MUID:70207560

A:Accession: A90249

A:Molecule type: protein

A:Residues: 1-30;81-326 <PIN>

C:Genetics:

A:Gene: GDB:IGHG4

A:Cross-references: GDB:119340; OMIM:147130
 A:Map position: 14q32.33-14q32.33

A:Introns: 99/1; 111/1; 221/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (lambda) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger aggregates.

C:Superfamily: Immunoglobulin C region; immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:134-203/Domain: immunoglobulin homology <IM2>

F:240-307/Domain: immunoglobulin homology <IM3>

F:14/Disulfide bonds: Interchain (to light chain) #status experimental

F:27-83,141-201,247-305/Disulfide bonds: #status predicted

F:106,109/Disulfide bonds: Interchain (to heavy chain) #status experimental

F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 63.5%; Score 1599.5; DB 1; Length 327;

Best Local Similarity 91.8%; Pred. No. 4e-84;

Matches 303; Conservative 9; Mismatches 15; Indels 3; Gaps 1;

QY 141 ASTKGPSVFPLAPSSKSTSGTAAALCLVDPPEPVTWNSGALTSGVHTFPAVLQSS 200

Db 1 ASTKGPSVFPLAPSSKSTSGTAAALCLVDPPEPVTWNSGALTSGVHTFPAVLQSS 60

QY 201 GLYSLSSVTVVPSSSLGTQTYICNVNHPKSNKVDKRVKPKSCDKTHTCPPCAPELLGG 260

Db 61 GLYSLSSVTVVPSSSLGTQTYICNVNHPKSNKVDKRVKPKSCDKTHTCPPCAPELLGG 260

QY 261 PSVFLPPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNKATKPREQYN 320

Db 118 PSVFLPPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNKATKPREQYN 320

QY 321 STYRVSVLVTLVHODWLNKEYCKVSNKALPAPIETKISKAKGQPREPOVYTLPPSREE 380

Db 178 STYRVSVLVTLVHODWLNKEYCKVSNKALPAPIETKISKAKGQPREPOVYTLPPSREE 380

QY 381 MTKNQVSLTCLVGFPSDIAVWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 440

Db 238 MTKNQVSLTCLVGFPSDIAVWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 440

QY 441 QQGNVFCSCVHHEALHNHYTQKSLSLSPGK 470

Db 298 QQGNVFCSCVHHEALHNHYTQKSLSLSPGK 327

RESULT 7

C2MS11

Ig gamma-2b chain - mouse

C:Species: Mus musculus (house mouse)

C:Date: 31-Mar-1980 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000

C:Accession: S25057; A02157; A26235; A26233; A53598

R:Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.

submitted to the EMBL Data Library, July 1992

A:Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific

A:Reference number: S25057

A:Accession: S25057

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-474 <FIS>

A:Cross-references: EMBL:X67210; NID:g54826; PIDN:CAA47649.1; PID:g54827

R:Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.

Nature 283, 786-789, 1980

A:Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from

A:Reference number: A02157; MUID:80120716

A:Contents: a allele

A:Accession: A02157

A:Molecule type: DNA

A:Residues: 138-161, 'L', 163-189, 'Fp', 193-474 <YAM>

A:Cross-references: GB:J00461

A:Note: the sequence was determined from the germline gene

R:Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.

Science 206, 1299-1303, 1979

A>Title: Structure of the constant and 3' untranslated regions of the murine gamma2b heavy chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

A:Reference number: A26235; MUID:80081501

A:Contents: MPC 11

A:Accession: A26235

A:Molecule type: mRNA

A:Residues: 138-172,'P',174-189,'FP',193-376,'T',378-474 <TU1>

A>Note: Lys-474 is probably renewed posttranslationally

R:Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R. Science 206, 1303-1306, 1979

A>Title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglobulin

A:Reference number: A26232; MUID:80081502

A:Accession: A26232

A:Molecule type: DNA

A:Residues: 138-172,'P',174-189,'FP',193-376,'T',378-474 <TU2>

R:Oillo, R.; Rougeon, F. Nature 296, 761-763, 1982

A>Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamma2b

A:Reference number: A26233; MUID:82173203

A:Accession: A26233

A:Contents: b allele

A:Molecule type: DNA

A:Residues: 138-161,'L',163-189,'FP',193-300,'R',302-331,'A',333-437,'DI',440-474 <OLL>

A:Cross-references: GB:J00461

R:Kim, H.; Yamauchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahashi, J. Biol. Chem. 269, 12345-12350, 1994

A>Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.

A:Reference number: A53598; MUID:94216359

A:Accession: A53598

A>Status: preliminary

A:Molecule type: protein

A:Residues: 234-251 <KM>

C:Comment: The a allele sequence is shown.

C:Genetics:

A:Introns: 138/1; 236/1; 258/1; 368/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (lambda) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin F;157-222/Domain: immunoglobulin homology <IM1>

F:236-257/Region: hinge

F:281-350/Domain: immunoglobulin homology <IM2>

F:387-454/Domain: immunoglobulin homology <IM3>

F:152/Disulfide bonds: interchain (to light chain) #status predicted

F:164-220,288-348,394-452/Disulfide bonds: #status predicted

F:247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicted

F:324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 61.4%; Score 1546; DB 1; Length 474;

Best Local Similarity 61.2%; Pred. No. 6.7e-81;

Matches 292; Conservative 67; Mismatches 108; Indels 10; Gaps 3;

QY 1 MGNSCIILFLVATATGVHRSOVQLVGSGAEVKKPCASVKVSKASGYTFTTYYWQWQKAP 60

DB 1 MEWSWIFLLSGTAGVHSEVQQSGPELVNPGASVKMSCKASGYTFTTYVHWVKQKP 60

QY 61 GQGLEWAGEIDPSDSTYNYNQKFKRATLVDTSTAYMELSLRSEDATVYYCARNRD 120

DB 61 GQGLEWIGYINPKDGTGKFKRATLTSKSSNTAYMELSLTSEDSAVYYCARDYD 120

QY 121 YSNWYFDVWEGEGLTVTVSSASTKGPVFPPLAPSSKSTSGTGAALGLVKDYFPEPVTS 180

DB 121 YD---WPAYWGQGLTVTVSSAAKTPPSVYPLAPCGDGTGSSVTSGCLVKGYEPESVTVT 177

QY 181 WNSGALTSGVHTTTPAVLOSGLYSLSSVTVVPSSSLGTQYIYNVHKPNTKVDKRVEP 240

DB 178 WNSGSLSSVHTTTPSQAALLQSLYTVSSSVTVSPSTWPSQTVCVAHPASSTTVDKKLEP 237

QY 241 KSCDKT--HTCPK-----CPAPELLGGPSVFLPCKPKDTLMISRTPEVTCVVVDVSHED 293

DB 238 SGPISTINCPCKECKCHKCPAPNLGGPSVFIIPPNIKQVLMISLTPKVKTVVVDVSEDD 297

QY 294 PEVKFNWYDGVGEVHNNAKTKPREEQYNSTYRVYSLVTLVHDLNKGKEYKCKVSNKALPA 353

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Db      298 PDVOISWFWNVVHTTQTQTHREDYNTSTIRVSVTLPIQHQQWMSGKEFKCKVNNKOLPS 357
      QY      354 PIEKTISKAKGPREPOVYTLPPSREBWTNQVSLTCLVKGFYPSDITAVESWGQEPENN 413
      Db      358 PIERTISKIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVGFNPGDTSVEMTNGHTEEN 417
      QY      414 YKTPPPVLDSDGSFPLYSKLTVDKSRWQQGVNFSCSYMHEALHNHYTKQSLSLSPGK 470
      Db      418 YKDTAPVLDSDGSFYIYKLNMTKSKWEKTDSPSCNVRHEGLKNYLLKKTISRSPGK 474

RESULT      8
S40295
Ig gamma-2a chain (mAb735) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
C:Accession: S40295
Submitted by: Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.;
A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 again
A:Reference number: S40295
A:Accession: S40295
A:Molecule type: protein
A:Residues: 1-446 <KLE>
C:Genetics:
A:Map position: 12
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: disulfide bond; glycoprotein; immunoglobulin; proglutamic acid
F:1-446/Product: Ig gamma-2a chain #status experimental <MAY>
F:1-117/Domain: V-D-J region <VDJ>
F:118-446/Domain: C region <CHR>
F:118-214/Domain: C1 region <CH1>
F:215-230/Region: Hinge
F:231-340/Domain: C2 region <CH2>
F:341-446/Domain: C3 region <CH3>
F:360-427/Domain: immunoglobulin homology <IMM>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:22-96,144-199,261-321,367-425/disulfide bonds: #status predicted
F:132/disulfide bonds: interchain (to light chain) #status predicted
F:224,227,229/disulfide bonds: interchain #status predicted
F:237/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match      61.3%; Score 1544; DB 2; Length 446;
Best Local Similarity 64.4%; Pred. No. 8.1e-81;
Matches 291; Conservative 59; Mismatches 94; Indels 8; Gaps 4;

QY      20 QVQLVQSGAEYKPKGASVKSCASGYFTFSYMQWYKQAPGGQLEWGEIDPSDSYTN 79
      Db      1 QIQLLQSGPELVRPGASVKISCSASGYFTFDYVIHWVKRQPGEGLEWIGWYPCSGN 60
      QY      80 NQRFKGRATLTVDTSTSTAYWEISSLSESDTAYYICARNRDYSNWYFDVWGEGTLVTVS 139
      Db      61 NEKFGRATLTVDTSSTAYMQLSSLTSEDSAVYFCARGKFA---MDYWGOGTSYTVS 116
      QY      140 SASTKGPSVEPLAPSSKTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQS 199
      Db      117 SAKTTAPSVPLAPVCGDTTGGSSVTLGCLVKGFPEPTVLTWNSGSLSSGVTHTFPAVLQS 176
      QY      200 SGLYSLSVVYTFVSSSLGTQTYICNVNHPKNTKVDKRVEPKSCDKTHTCTPP--CPAPEL 257
      Db      177 D-LYTLSSVYTVTSSTWPSQSITCNVAHPASSTKVDKIEPRG-PTIKPCPCCKCAPNL 234
      QY      258 LGGSPVLFPPKPKDPTLMIKRTPEVTCVVVDVSHEDDEVFKPNVYGVGVHNAKTKPRE 317
      Db      235 LGGSPVIFPPKIKDKVLMISLSPMTCCVVVDVSDDDPDVQISWFNVNVEVLTAQTQTHRE 294
      QY      318 QYNSTYRVVSVLTVLHDWLNKREYKCKVSKNALPALPIEKTISKAKQPREPOVYTLPPS 377
      Db      295 DYNSTLRWVALPTIQHQQWMSGKEFKCKVNNKOLPAPIERTISKPKGSVRAPVYVLPPP 354
      QY      378 REEMTKNOVSLTCLVKGFYPSDITAVESWGQEPNNYKTTTPPVLDSDGSFPLYSKLTVDV 437

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Db 355 EEEMTKQVILTCMTDFMPEDIVVETNNGKTELNTKTEPVLDSGSGFMYSKLRVEK 414
Qy 438 SRWQGNVFCSCVMHEALHNHYTKQSLSPG 469
Db 415 KNWVERNSYSCSVVHGLEHNNHTTKSFSTRPG 446

RESULT 9
S01321
Ig gamma-2b chain precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
C:Accession: S01321
R:de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
Eur. J. Biochem. 176, 287-295, 1988
A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed a
A:Reference number: S01320; MUID:88329081
A:Accession: S01321
A:Molecule type: mRNA
A:Residues: 1-475
A:Cross-references: EMBL:X13188; NID:g51780; PIDN:CAA31580.1; PID:g51781
A:Note: this sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-475/Product: Ig gamma-2b chain #status predicted <MAT>
F:159-223/Domain: immunoglobulin homology <IMM>

Query Match 59.7%; Score 1501.5; DB 2; Length 475;
Best Local Similarity 60.6%; Pred. No. 2.3e-78;
Matches 289; Conservative 66; Mismatches 113; Indels 9; Gaps 4;

Qy 1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVKASGVTFTSYMMQWVKQAP 60
Db 1 MEWITWFLFILSGTAGVQSQVQLQSGAEIARPGASVKLSCKASGYTLTIGISWVKQT 60
Qy 61 GQLEWMGEIDPSDSTYNNQKFKGKATLVDTSTAYMELSSLRSEDTAVTYICARNRD 120
Db 61 GQGLEWIGEYIPGSGNSYFNEKEFKGKATLVDKSSSTAYLHLSLTSEDSAVYFCAGPRQ 120
Qy 121 YSNWVDFWVGEGLTVTSASATKGPSVFPLAPSSKTSSTGTAALGCLVKDYKPEPTVS 180
Db 121 V-GLLPFGYWGQGLTVTASAAKTPPSVPLAPGCGDTTGGSSVTLGCLVKGYFPESTVT 179
Qy 181 WNSGALTSGVHTTTPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKRVEP 240
Db 180 WNSGSLSSVHTTTPALLO-SGLYTMSSSVTVPSWTPSQVITCVSAHPASSTVDDKLEP 238
Qy 241 KSCDKT-HTCPCP-----CPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHED 293
Db 239 SGPTSTINPCPCCKECHKCAPNLEGGPSVFIFPPNKKDLMISLTPKVKTVVVDVSEDD 298
Qy 294 PEYKFNWYDGEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 353
Db 299 PDVQISWFMNVEVLAQTQTHREDYNSTIRVVSALPIQHQDWMSGEKFEKCKVNNKDLPA 358
Qy 354 PIEKTIKAKGQPREPOVYTPPPSRDEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENN 413
Db 359 PIERTISKIGIYRAQVQVYILSPPPQLSKRDKVSLTCLAVGFSPEDISVETWNGHTEEN 418
Qy 414 YKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTKQSLSPG 470
Db 419 YKDTAPVLDSDGSFYIYSKLNMTKSKWEKTDSPSCNVRHEGLKNYLYLKKTISSPGK 475

RESULT 10
S22080
Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine
N:Alternate names: Ig gamma-1 chain C region (clone 8.10)
C:Species: Bos primigenius taurus (cattle)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S22080; S06610; A31303
R:Sanders, P.G.
submitted to the EMBL Data Library, November 1991
A:Reference number: S22080
A:Accession: S22080
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-470 <SAN>
A:Cross-references: EMBL:X62916; NID:g439; PIDN:CAA44699.1; PID:g440
R:Symons, D.B.A.; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989
A:Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and g
A:Reference number: S06610; MUID:90097956
A:Accession: S06610
A:Molecule type: DNA
A:Residues: 142-470 <SYM>
A:Cross-references: EMBL:X16701
A:Note: the sequence was determined from the germline gene
C:Genetics:
A:Gene: Ig CH gamma-1
A:Introns: 98/1; 111/1; 221/1
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein
F:161-225/Domain: immunoglobulin homology <IMM>
F:318/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 58.4%; Score 1471; DB 2; Length 470;
Best Local Similarity 60.0%; Pred. No. 1.2e-76;
Matches 283; Conservative 64; Mismatches 115; Indels 10; Gaps 7;

Qy 3 WSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVKASGVTFTSYMMQWVKQAPGQ 62
Db 5 WT--LLFVLSAPIGVLSQVQLRESGPSLVKPSQTLSTCTVSGFSLSYALTWVRQAPGK 62
Qy 63 GLEWMGEIDPSDSTYNNQKFKGKATLVDTSTAYMELSSLRSEDTAVTYICARNR-D 120
Db 63 ALEWVGGI-TSGGTTYNNPALKSRLSITKENSQVSLSVSVTPEDTATYYCARSTYGE 121
Qy 121 YSNWVDFWVGEGLTVTSASATKGPSVFPLAPSSKTSSTGTAALGCLVKDYKPEPTVS 180
Db 122 VGGATADAWGQGLTVTSASATPAKVIPLSSCCGDKSSVTVLGCLVSSYMPPEPTVT 181
Qy 181 WNSGALTSGVHTTTPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKRVEP 240
Db 182 WNSGALKSGVHTTTPAVLQSSGLYSLSSVTVTPGSTG-QTFTCNVAHPASSTKVDKAVDP 240
Qy 241 KSCDKTHTCPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
Db 241 -TC-KPSPCCCPPELPGGPSVFIFPPKPKDTLTISGTPETVTCVVVDVGHDDPEVKFSW 298
Qy 301 YVDGVEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
Db 299 FVDDVEVNTATTPREEQFNSTIRVVSALRIQHQDWTCGKEFKCKVHNEGLPAPIVRTIS 358
Qy 361 KAKGQPREPOVYTPPPSRDEMTKNQVSLTCLVKGFYPSDIAVWESNGQP--ENNYKTP 418
Db 359 RTKGPAEPQVYVLAPEQELSKSTVSLTCMVTSTFYPDYIAVEMQRNGQPESEDKYGTTP 418
Qy 419 PVLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTKQSLSPGK 470
Db 419 PQLDASSVFLYSLKLRVDRNSWQEGDTYTCVVMHEALHNHYTKQSKSAGK 470

RESULT 11
S31459
Ig gamma-1 chain - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C:Accession: S31459
R:Patric, S.; Nau, F.
submitted to the EMBL Data Library, December 1992
A:Reference number: S31459

A:Accession: S31459
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-472 <PAT>
A:Cross-references: EMBL:X69797
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:277-346/Domain: immunoglobulin homology <IMM>

Query Match 58.3%; Score 1467; DB 2; Length 472;
Best Local Similarity 59.4%; Pred. No. 2.1e-76;
Matches 282; Conservative 67; Mismatches 114; Indels 12; Gaps 6;

Qy 3 WSCIILFVATATGVHSGVOLVSGAEVKKPGASVKVSKASGTYFTTSYWMQVKAQPGQ 62
Db 3 WT--LLEFVAPRGVLSQVRLQESGSLATLQTLSTVCTISGSLNNGVDVWQAQPGK 60
Qy 63 GLEWMGEIDPDSYNTYNOKEKGRATLVDTSTAYMELSSLRSEDYAVYVCARNRYS 122
Db 61 ALEWLG--SGYDEDIDYNPVLKSLSTKDKSKQVSLTSLTVTTEDYAVYCAR-VDYD 118
Qy 123 NNWYF-----DWGEGTLTVYSSASTKGPSVFPLAPSSKSTSGGTAALGCLVDFPEPV 177
Db 119 SSHAFAYASYDFWGPGLLISVLSASTPPKVPYPLTSCCGDTSSSIIVTLGCLVSSYMPPEV 178
Qy 178 TVSNWNGALTSVHTFPFVAVLSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKYDKR 237
Db 179 TVTNWNGALTSVHTFPFVAVLSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKYDKR 238
Qy 238 VEPKSCDKTHPCPCPAPPELLGGSVFPPKPKDITLMISRTPEVTVVVDVSHEDPEVK 297
Db 239 VEPGCPDCKHC-RCPPPELPGGSVFPPKPKDITLMISRTPEVTVVVDVSHEDPEVK 297
Qy 298 FNWYVDGVHNAKTTPREEQNSTYRVSVLTVLHODWLGKKEYCKVSKNKAAPAPTEK 357
Db 298 FSWFVDNVEVARTKPREEQNFSTFVVSALPIQHQDWTGCKEKKCKVNEALPAPIVR 357
Qy 358 TISRAKQGPPEPVYVTLPPSREMTKNOVSLTCLVKGYPDSIAVWESNGQP--ENNYK 415
Db 358 TISRTKGAREPVYVTLPPSREMTKNOVSLTCLVKGYPDSIAVWESNGQP--ENNYK 417
Qy 416 TTPPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSLSPGK 470
Db 418 TTSQLDADGSFFLYSLRLVDKNWQEGDTYACVVMHEALHNHYTKSLSLSPGK 472

RESULT 12
PC4436
monoclonal antibody 13-1 heavy chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C:Accession: PC4436
R:Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.
Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyrin
A:Reference number: JC5810; MUID:98063277
A:Accession: PC4436
A:Molecule type: protein
A:Residues: 1-444 <AKA>
C:Comment: This catalytic antibody has peroxidase oxidase activity. It is directed against
F:251-320/Domain: immunoglobulin homology <IMM>
F:22/Disulfide bonds: interchain (to 98) #status predicted
F:99/Disulfide bonds: interchain (to 109) #status predicted

Query Match 56.9%; Score 1432.5; DB 2; Length 444;
Best Local Similarity 57.5%; Pred. No. 1.7e-74;
Matches 263; Conservative 81; Mismatches 94; Indels 19; Gaps 8;

Qy 20 QVOLVSGAEVKKPGASVKVSKASGTYFTTSYWMQVKAQPGQGLEWMGEID-PSDSY-T 77
Db 20 QVOLVSGAEVKKPGASVKVSKASGTYFTTSYWMQVKAQPGQGLEWMGEID-PSDSY-T 77

Db 1 EVQXVETGGGLVPCNSLKLCLTSGFTFSNRYMHHLRQPPCKRLWIAVITVKSNDYCA 60
Qy 78 NYNQKFKGKATLVDTSTAYMELSSLRSEDYAVYVCARNRDYNNWYF--DWNGEGTL 135
Db 61 KYAESVGRGRTISRDDSKSSVYLOMNLREEDYATVYCCR-----TPWYVAMDCWQGGTS 115
Qy 136 VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVDFPEPVTVSNWNGALTSVHTFPA 195
Db 116 VTVSSAKTTPPSVYPLAPGSAQTNSMTVLGCLVKGYPPEPVTVSNWNGALTSVHTFPA 175
Qy 196 VLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKDKRVEPKSCDKTHTCP--CP 253
Db 176 VLQSD-LYTLSSSVTVPPSSSLGTQTYICNVNHNKPSNTKDKRVEPKSCDKTHTCP--CP 230
Qy 254 APELLGGPSVFLPDKPKDITLMISRTPEVTVVVDVSHEDPEVKFNWYVDGVVEVINAKTK 313
Db 231 VPEV---SSVFIFPPKPKDITLTLPKTVVVDVSHEDPEVKFNWYVDGVVEVINAKTK 287
Qy 314 PREEQNSTYRVSVLTVLHODWLGKKEYCKVSKNKAAPAPTEKTSKAKGQPREPVYT 373
Db 288 PREEQNSTYRVSVLTVLHODWLGKKEYCKVSKNKAAPAPTEKTSKAKGQPREPVYT 347
Qy 374 LPPSREMTKNOVSLTCLVKGYPDSIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKL 433
Db 348 IPPPKQMAKDKVSLTCLVKGYPDSIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKL 407
Qy 434 TVDKSRWQGNVFCSCVMHEALHNHYTKSLSLSPGK 470
Db 408 NVQKSNWEGAGTTCVSLHGLHNNHTEKSLSHSPGK 444

RESULT 13
S69339
Ig heavy chain V region precursor - human
C:Species: Homo sapiens (man)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C:Accession: S69339; S72664
R:Khamilich, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A:Reference number: S69339; MUID:95262687
A:Accession: S69339
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <KHA>
A:Cross-references: EMBL:X81695
R:Khamilich, A.A.
submitted to the EMBL Data Library, September 1994
A:Reference number: S72664
A:Accession: S72664
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140, 'C', 142-374 <KH2>
A:Cross-references: EMBL:X81695
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 56.8%; Score 1429; DB 2; Length 374;
Best Local Similarity 59.7%; Pred. No. 2.3e-74;
Matches 280; Conservative 29; Mismatches 58; Indels 102; Gaps 4;

Qy 5 CIIILFVATATGVHSGVOLVSGAEVKKPGASVKVSKASGTYFTTSYWMQVKAQPGQ 62
Db 5 CSTLLLTIPSWLSQITLKESGPTLVKPTQTTLCTFSGFSKLSGVGVGWIROPQ 64
Qy 63 GLEWMGEIDPDSYNTYNOKEKGRATLVDTSTAYMELSSLRSEDYAVYVCARN-RDY 121
Db 65 ALEWLIIFWDDD-KRYSPLKTRITITADTSKNQVLTMTNVDPADTATYCGSVSEY 123
Qy 122 SNWYFDVWEGEGLTVVTSASSTKGPSVFPLAPSSKSTSGGTAALGCLVDFPEPVTVSW 181
Db 124 GQGYRFSWGGTTLTVSS----- 142

QY 182 NSGALTSVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKRVPEPK 241
Db 143 -----EPK 145
QY 242 SCDKTHTCPCPAPELGGPSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWY 301
Db 146 SCDKTHTCPCPAPELGGPSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWY 205
QY 302 VDGVEVHNATKPREQNTYRVSIVLTVLHODWLNKGEYCKVSNKALPAPIETKISK 361
Db 206 VDGVEVHNATKPREQNTYRVSIVLTVLHODWLNKGEYCKVSNKALPAPIETKISK 265
QY 362 AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 421
Db 266 AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 325
QY 422 DSDGSFELYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTOKSLSPGK 470
Db 326 DSDGSFELYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTOKSLSPGK 374

RESULT 14

I47159

Ig gamma 2a chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47159
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845
A:Accession: I47159
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124
C:Genetics:
A:Gene: IgG2a
C:Superfamily: Immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: Immunoglobulin homology <IMM>

Query Match 50.3%; Score 1267; DB 2; Length 328;
Best Local Similarity 69.9%; Pred. No. 3.1e-65;
Matches 232; Conservative 42; Mismatches 52; Indels 6; Gaps 2;

QY 141 ASTKGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVWSNNSGALTSGVHTFPAVLQSS 200
Db 1 APTAPSVPLAPCSRDTSGPNVALGLASSYPPEPTVTWNSGALSSGVHTFPSVLQPS 60
QY 201 GLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKRVPEKSCDKTHTCPCPAPELLGG 260
Db 61 GLYSLSSMTVPASSLSKSYTCNVNHPATTTKVDKRVGKTTPCPICPACESP----G 116
QY 261 PSVFLPPPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 320
Db 117 PSVFIIPPCKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHTAQTREKESQFN 176
QY 321 STYRVSVLTVLHODWLNKGEYCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSREE 380
Db 177 STYRVSVLPIQHODWLNKGEYCKVSNKALPAPIETRIISKAKGQTPREPOVYTLPPHAE 236
QY 381 MTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGSFFLYSKLTVDKS 438
Db 237 LRSKSVSITCLVIGFYPPDIDVEMQRNGQPEEGNRTTPPQQQVDGTYFLYSKFSVDKA 296
QY 439 RWQGNVFCSCVMHEALHNHYTOKSLSPGK 470
Db 297 SWQGGGIFQCAVMHEALHNHYTOKSISKTPGK 328

RESULT 15

I47160

Ig gamma 2b chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47160
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of
A:Reference number: I47158; MUID:95015845
A:Accession: I47160
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PID:g433126
C:Genetics:
A:Gene: IgG2b
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: Immunoglobulin homology <IMM>

Query Match 50.1%; Score 1261; DB 2; Length 328;
Best Local Similarity 69.6%; Pred. No. 6.9e-65;
Matches 231; Conservative 41; Mismatches 54; Indels 6; Gaps 2;

QY 141 ASTKGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVWSNNSGALTSGVHTFPAVLQSS 200
Db 1 APTAPLVPLAPCGRDTSGPNVALGLASSYPPEPTVTWNSGALTSGVHTFPSVLQPS 60
QY 201 GLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKRVPEKSCDKTHTCPCPAPELLGG 260
Db 61 GLYSLSSMTVPASSLSKSYTCNVNHPATTTKVDKRVGKTTPCPICPACESP----G 116
QY 261 PSVFLPPPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYN 320
Db 117 PSVFIIPPCKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHTAQTREKESQFN 176
QY 321 STYRVSVLTVLHODWLNKGEYCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSREE 380
Db 177 STYRVSVLPIQHODWLNKGEYCKVSNKALPAPIETRIISKAKGQTPREPOVYTLPPHAE 236
QY 381 MTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGSFFLYSKLTVDKS 438
Db 237 LRSKSVSITCLVIGFYPPDIDVEMQRNGQPEEGNRTTPPQQQVDGTYFLYSKFSVDKA 296
QY 439 RWQGNVFCSCVMHEALHNHYTOKSLSPGK 470
Db 297 SWQGGGIFQCAVMHEALHNHYTOKSISKTPGK 328

Search completed: April 17, 2002, 16:39:54
Job time: 167 sec

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OM protein - protein search, using sw model

Run on: April 17, 2002, 16:41:04 ; Search time 17.09 Seconds
(without alignments)
1008.336 Million cell updates/sec

Title: US-09-499-662-117

Perfect score: 2517

Sequence: 1 MGVSCILLFLVATATGVHQS.....MHEALNHVYTKSLSPCK 470

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1758	69.8	330	1 GCL_HUMAN	P01857 homo sapien
2	1610	64.0	326	1 GC2_HUMAN	P01859 homo sapien
3	1599.5	63.5	327	1 GC4_HUMAN	P01861 homo sapien
4	1231.5	48.9	323	1 CC_RABIT	P01870 oryctolagus
5	1210.5	48.1	329	1 GC2_CAVPO	P01862 cavia porce
6	1162	46.2	290	1 GC3_HUMAN	P01860 homo sapien
7	1155	45.9	326	1 GC1_RAT	P20759 rattus norv
8	1150	45.7	329	1 GC3_MOUSE	P22436 mus musculu
9	1145	45.5	324	1 GC1_MOUSE	P01868 mus musculu
10	1144.5	45.5	333	1 GCB_RAT	P20761 rattus norv
11	1140	45.3	333	1 GCL_MOUSE	P01869 mus musculu
12	1139	45.3	398	1 GC3_MOUSE	P03987 mus musculu
13	1129	44.9	330	1 GCAA_MOUSE	P01863 mus musculu
14	1127.5	44.8	329	1 GCC_RAT	P20762 rattus norv
15	1126.5	44.8	335	1 GCAB_MOUSE	P01864 mus musculu
16	1124	44.7	399	1 GCAM_MOUSE	P01865 mus musculu
17	1115	44.3	322	1 GCB_RAT	P20760 rattus norv
18	1085	43.1	336	1 GCB_MOUSE	P01866 mus musculu
19	1080	42.9	405	1 GCB_MOUSE	P01867 mus musculu
20	559.5	22.2	139	1 HV07_MOUSE	P01751 mus musculu
21	528	21.0	117	1 HV06_MOUSE	P01750 mus musculu
22	521.5	20.7	137	1 HV11_MOUSE	P01755 mus musculu
23	521	20.7	138	1 HV48_MOUSE	P03980 mus musculu
24	516	20.5	117	1 HV05_MOUSE	P01749 mus musculu
25	507	20.1	140	1 HV02_MOUSE	P01746 mus musculu
26	504	20.0	117	1 HV09_MOUSE	P01753 mus musculu
27	491	19.5	117	1 HV04_MOUSE	P01748 mus musculu
28	488	19.4	117	1 HV49_MOUSE	P06328 mus musculu
29	486.5	19.3	429	1 EPC_RAT	P01855 rattus norv
30	486	19.3	428	1 EPC_HUMAN	P01854 homo sapien
31	482	19.1	117	1 HV10_MOUSE	P01754 mus musculu
32	479	19.0	136	1 HV15_MOUSE	P01759 mus musculu
33	477	19.0	117	1 HV16_HUMAN	P23083 homo sapien

34	471	18.7	421	1 EPC_MOUSE	P06336 mus musculu
35	467	18.6	117	1 HV1B_HUMAN	P01743 homo sapien
36	460	18.3	117	1 HV12_MOUSE	P01756 mus musculu
37	459	18.2	117	1 HV13_MOUSE	P01757 mus musculu
38	457.5	18.2	147	1 HV1C_HUMAN	P01744 homo sapien
39	454.5	18.1	120	1 HV50_MOUSE	P06329 mus musculu
40	448	17.8	120	1 HV03_MOUSE	P01747 mus musculu
41	446.5	17.7	455	1 MUC_MOUSE	P01872 mus musculu
42	445	17.7	454	1 MUC_HUMAN	P01871 homo sapien
43	439	17.4	458	1 MUC_RABIT	P03988 oryctolagus
44	438	17.4	121	1 HV01_MOUSE	P01745 mus musculu
45	436.5	17.3	476	1 MUCM_MOUSE	P01873 mus musculu

ALIGNMENTS

RESULT 1					
1	GCL_HUMAN				
ID	GCL_HUMAN	STANDARD;	PRT;	330 AA.	
AC	P01857;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	IG GAMMA-1 CHAIN C REGION.				
GN	IGHG1.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=82274238; PubMed=6287432;				
RA	Ellison J.W., Berson B.J., Hood L.E.;				
RT	"The nucleotide sequence of a human immunoglobulin C gamma1 gene."				
RL	Nucleic Acids Res. 10:4071-4079(1982).				
RN	[2]				
RP	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).				
RX	MEDLINE=71064024; PubMed=3489771;				
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,				
RA	Waxdal M.J., Edelman G.M.;				
RT	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino				
RT	acid sequence of heavy-chain cyanogen bromide fragments H1-H4."				
RL	Biochemistry 9:3161-3170(1970).				
RN	[3]				
RP	SEQUENCE OF 136-329 (EU).				
RX	MEDLINE=71064025; PubMed=5530842;				
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,				
RA	Edelman G.M.;				
RT	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino				
RT	acid sequence of heavy-chain cyanogen bromide fragments H5-H7."				
RL	Biochemistry 9:3171-3181(1970).				
RN	[4]				
RP	SEQUENCE (MYELOMA PROTEIN NIE).				
RX	MEDLINE=77070269; PubMed=826475;				
RA	Ponstingl H., Hilschmann N.;				
RT	"The rule of antibody structure. The primary structure of a				
RT	monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The				
RT	chymotryptic peptides of the H-chain, alignment of the tryptic				
RT	peptides and discussion of the complete structure."				
RL	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).				
RN	[5]				
RP	SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.				
RX	MEDLINE=83289131; PubMed=684994;				
RA	Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;				
RT	"Three-dimensional structure determination of antibodies. Primary				
RT	structure of crystallized monoclonal immunoglobulin IgG1 KOL, I."				
RL	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).				
RN	[6]				
RP	DISULFIDE BONDS.				
RX	MEDLINE=71064027; PubMed=4923144;				
RA	Gall W.E., Edelman G.M.;				
RT	"The covalent structure of a human gamma G-immunoglobulin. X.				

RT Intrachain disulfide bonds.":
 RL Biochemistry 9:3188-3196(1970).
 RN [7]
 RX DISULFIDE BONDS.
 RX MEDLINE=77070267; PubMed=1002129;
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.:
 RA "Rule of antibody structure. The primary structure of a monoclonal
 RT IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
 RT characterization of the protein, the L- and H-chains, the
 RT cyanogen bromide cleavage products, and the disulfide bridges.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE=81208100; PubMed=7236608;
 RA Deisenhofer J.:
 RA "Crystallographic refinement and atomic models of a human Fc fragment
 RT and its complex with fragment B of protein A from Staphylococcus
 RT aureus at 2.9- and 2.8-A resolution.";
 RL Biochemistry 20:2361-2370(1981).
 CC -1- MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE
 CC GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3)
 CC MARKER & THE GIM (NON-1) MARKERS.
 CC -1- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
 CC 35,116,198,269 & 272.
 CC -1- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
 CC 155, 166, 177, 199, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
 CC 268-272.
 CC -1- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
 CC RESIDUES 198,267&272.
 CC -----
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 DR EMBL; J00228; AAC82527.1; AUT_INIT.
 DR FIR; A02146; GHU.
 DR PDB; 1FC1; 15-JUL-92.
 DR PDB; 1FC2; 15-JUL-92.
 DR MIM; 147100; -
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003597; Ig_C1.
 DR InterPro; IPR003600; Ig_Like.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00407; IgC1; 2.
 DR SMART; SM00410; Ig_Like; 1.
 DR PROSITE; PS00290; Ig_MHC; 2.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 3D-structure.
 FT NON_TER 1 1
 FT DOMAIN 1 98 CH1.
 FT DOMAIN 99 110 HINGE.
 FT DOMAIN 111 223 CH2.
 FT DOMAIN 224 330 CH3.
 FT DISULFID 27 83
 FT DISULFID 103 103 INTERCHAIN (WITH LIGHT CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).
 FT DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).
 FT DISULFID 144 204
 FT DISULFID 250 308
 FT CARBOHYD 180 180
 FT MOD_RES 330 330
 FT VARIANT 97 97
 FT VARIANT 239 239
 FT VARIANT 241 241
 FT STRAND 123 126
 FT HELIX 130 134
 N-LINKED (GLCNAC. . .).
 REMOVED POST-TRANSLATIONALLY.
 K -> R (IN GIM(3) MARKER).
 /FTId=VAR_003886.
 D > E (IN GIM(NON-1) MARKER).
 /FTId=VAR_003887.
 L -> M (IN GIM(NON-1) MARKER).
 /FTId=VAR_003888.

FT	TURN	136	137
FT	STRAND	141	148
FT	STRAND	158	162
FT	TURN	163	164
FT	STRAND	165	166
FT	STRAND	175	178
FT	STRAND	183	190
FT	HELIX	193	197
FT	TURN	198	199
FT	STRAND	202	206
FT	STRAND	215	219
FT	STRAND	227	227
FT	STRAND	230	234
FT	HELIX	238	240
FT	TURN	241	242
FT	STRAND	245	256
FT	STRAND	260	266
FT	TURN	267	268
FT	STRAND	269	270
FT	STRAND	274	276
FT	STRAND	280	281
FT	TURN	283	284
FT	STRAND	287	296
FT	HELIX	297	301
FT	TURN	302	303
FT	STRAND	306	312
FT	TURN	313	314
FT	TURN	316	317
FT	STRAND	320	324
SQ	SEQUENCE	330 AA; 36106 MW; 3770EE106C2FA33D CRC64;	

Query Match 69.8%; Score 1758; DB 1; Length 330;
 Best Local Similarity 99.1%; Pred. No. 9.9e-114; Indels 0; Gaps 0;
 Matches 327; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY	141	ASTKGSVFPLAPSSKSTSGTAAALCLVKDYDPEPVTVSVNSGALTSGVHTFPAVLQSS	200
DB	1	ASTKGSVFPLAPSSKSTSGTAAALCLVKDYDPEPVTVSVNSGALTSGVHTFPAVLQSS	60
QY	201	GLYSLSSVTVPPSSSLGTQYICNVNHPKSTKVKDKVPEKSCDKHTCPCPAPELLGG	260
DB	61	GLYSLSSVTVPPSSSLGTQYICNVNHPKSTKVKDKVPEKSCDKHTCPCPAPELLGG	120
QY	261	PSVFLPPPKDLMISRTPEVTCVVDVSHEDPEVKFNNYVDGVEVHNNAKTPREEQYN	320
DB	121	PSVFLPPPKDLMISRTPEVTCVVDVSHEDPEVKFNNYVDGVEVHNNAKTPREEQYN	180
QY	321	STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDE	380
DB	181	STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDE	240
QY	381	MTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW	440
DB	241	LTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW	300
QY	441	QQGNVFSCSVMHEALHNHYTQKSLSLSPGK	470
DB	301	QQGNVFSCSVMHEALHNHYTQKSLSLSPGK	330

RESULT 2
 GC2_HUMAN
 ID GC2_HUMAN STANDARD; PRT; 326 AA.
 AC P01859;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE IG GAMMA-2 CHAIN C REGION.
 GN IGHG2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82197621; PubMed=6804948;
RA Ellison J.W., Hood L.E.;
RT "Linkage and sequence homology of two human immunoglobulin gamma
RL heavy chain constant region genes.";
RN Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
[2]
RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
RX MEDLINE=81007873; PubMed=6774012;
RA Wang A.-C., Tung E., Fudenberg H.H.;
RT "The primary structure of a human IgG2 heavy chain: genetic,
RL evolutionary, and functional implications.";
RN J. Immunol. 125:1048-1054(1980).
[3]
RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
RX MEDLINE=80001357; PubMed=113060;
RA Connell G.E., Parr D.M., Hofmann T.;
RT "The amino acid sequences of the three heavy chain constant region
RL domains of a human IgG2 myeloma protein.";
RN Can. J. Biochem. 57:758-767(1979).
[4]
RP SEQUENCE OF 238-275 (ZIE).
RX MEDLINE=80114419; PubMed=118920;
RA Hofmann T., Parr D.M.;
RT "A note of the amino acid sequence of residues 381-391 of human
RL immunoglobulins gamma chains.";
RN Mol. Immunol. 16:923-925(1979).
[5]
RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
RX Hofmann T., Parr D.M.;
RT Submitted (MAR-1980) to the PIR data bank.
[6]
RP SEQUENCE OF 1-121 (DOT).
RX MEDLINE=95255298; PubMed=7737190;
RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RT "Characterization of the two unique human anti-flavin monoclonal
RL immunoglobulins.";
RN Eur. J. Biochem. 228:886-893(1995).
[7]
RP DISULFIDE BONDS.
RX MEDLINE=72033500; PubMed=4940472;
RA Milstein C., Frangione B.;
RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
RN Biochem. J. 121:217-225(1971).
[8]
RP DISULFIDE BONDS.
RX MEDLINE=69064124; PubMed=5782707;
RA Frangione B., Milstein C., Pink J.R.L.;
RT "Structural studies of immunoglobulin G.";
RN Nature 221:145-148(1969).

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CC -----
DR EMBL: V00554; CAB58438.1; -;
DR PIR: A02148; G2HU.
DR MIM: 147110; -;
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig-cl.
DR InterPro: IPR003600; Ig-like.
DR Pfam: PF00047; Ig; 3.
DR SMART: SM00407; Igc1; 2.
DR SMART: SM00410; Ig-like; 1.
DR PROSITE: PS00290; IG_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region.
RN NON_TER 1 1

FT DOMAIN 1 98 CH1.
FT DOMAIN 99 110 HINGE.
FT DOMAIN 111 219 CH2.
FT DOMAIN 220 326 CH3.
FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 83 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 103 103 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 140 200 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 246 304
FT SITE 156 156
FT MOD_RES 326 326
FT VARIANT 60 60
SQ SEQUENCE 326 AA; 35884 MW; 8310878C6878CF9C CRC64;
Query Match 64.0%; Score 1610; DB 1; Length 326;
Best Local Similarity 91.8%; Pred. No. 1.4e-103;
Matches 303; Conservative 10; Mismatches 13; Indels 4; Gaps 2;
QY 141 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
DB 1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 201 GLYSLSSVTVFSSSLGTQTYICNVNHKPSNTKYVDKRVKPSCKDHTHTCPPCPAPELGG 260
DB 61 GLYSLSSVTVFSSNFGTQTYTCNVDHKPSNTKYVDKRVKPSCKDHTHTCPPCPAPELGG 116
QY 261 PSVELFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKENWYVDGVEVINAKTKPREEQYN 320
DB 117 PSVELFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKENWYVDGVEVINAKTKPREEQFN 176
QY 321 STYRVSVTLTVLHODWLNKGYCKVKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE 380
DB 177 STYRVSVTLTVHODWLNKGYCKVKVSNKGLPAPIEKTISKAKGQPREPQVYTLPPSREE 236
QY 381 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 440
DB 237 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 296
QY 441 QGQNVFSCSVMEALHNHYTQKSLSLSPGK 470
DB 297 QGQNVFSCSVMEALHNHYTQKSLSLSPGK 326
RESULT 3
GC4_HUMAN
ID GC4_HUMAN STANDARD; PRT; 327 AA.
AC P01861;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE IG GAMMA-4 CHAIN C REGION.
GN IGHG4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83157104; PubMed=6299662;
RA Ellison J.W., Buxbaum J.N., Hood L.E.;
RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
RL DNA 1:11-18(1981).
RN [2]
RP SEQUENCE OF 1-30 AND 81-326.
RX MEDLINE=70207560; PubMed=4192699;
RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
RN constant region of a gamma 4 chain.";

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RL Biochem. J. 117:33-47(1970).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; K01316; AAB59394.1; ALT_INIT.
DR PIR; A02150; G4HU.
DR MIM; 147130; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IgC1; 2.
DR SMART; SM00410; Ig_Like; 1.
DR PROSITE; PS00290; IG_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DOMAIN 1 98 CH1.
FT DOMAIN 99 110 HINGE.
FT DOMAIN 111 220 CH2.
FT DOMAIN 221 327 CH3.
FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 83
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 141 201
FT DISULFID 247 305
SQ SEQUENCE 327 AA; 35940 MW; 3EDBD81EF208E7A CRC64;

Query Match 63.5%; Score 1599.5; DB 1; Length 327;
Best Local Similarity 91.8%; Pred. NO. 7.3e-103;
Matches 303; Conservative 9; Mismatches 15; Indels 3; Gaps 1;

QY 141 ASTKGPSVFLPAPSSKSTSGTAAAGCLVKDYFPEPTVTSWNSGALTSGVHTPFAVLQSS 200
Db 1 ASTKGPSVFLPAPSSKSTSGTAAAGCLVKDYFPEPTVTSWNSGALTSGVHTPFAVLQSS 60
QY 201 GLYSLSVTVTPSSSLGTQTYICNVNHKFSNTKVDKRVKPKSCDKTHTCPCPAPELGG 260
Db 61 GLYSLSVTVTPSSSLGTQTYICNVNHKFSNTKVDKRVKPKSCDKTHTCPCPAPELGG 117
QY 261 PSVFLFPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVVHNKATKPREEQYN 320
Db 118 PSVFLFPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVVHNKATKPREEQYN 177
QY 321 STYRVVSVLTVTLHQLDNLNGKEYCKYKSNKALPAPIETKISKAKGQPREPOVYTLPPSREE 380
Db 178 STYRVVSVLTVTLHQLDNLNGKEYCKYKSNKALPAPIETKISKAKGQPREPOVYTLPPSREE 237
QY 381 MTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVPLVSDGFFLYSKLTVDKSRW 440
Db 238 MTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVPLVSDGFFLYSKLTVDKSRW 297
QY 441 QGQNVFSCSMHREALNHVYTKQSLSLSPGK 470
Db 298 QGQNVFSCSMHREALNHVYTKQSLSLSPGK 327

RESULT 4
GC_RABIT
ID GC_RABIT STANDARD; PRT; 323 AA.
AC F01870;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG GAMMA CHAIN C REGION.
OS Oryctolagus cuniculus (Rabbit).

```

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN NCBI_TaxID=9986;
[1]
RX SEQUENCE FROM N.A.
RX MEDLINE=84030930; PubMed=6313520;
RA Bernstein K.E., Alexander C.B., Mage R.G.;
RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
RT F-1 haplotype.";
RL Immunogenetics 18:387-397(1983).
RN [2]
RX SEQUENCE OF 1-128.
RX MEDLINE=76135469; PubMed=1243651;
RA Pratt D.M., Mole L.E.;
RT "Sequence studies on the constant region of the Fd sections of rabbit
RT immunoglobulin G of different allotype.";
RL Biochem. J. 151:337-349(1975).
RN [3]
RX SEQUENCE OF 88-266 FROM N.A.
RX MEDLINE=83299917; PubMed=6193512;
RA Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
RT "Heavy chain genes of rabbit IgG: Isolation of a cDNA encoding gamma
RT heavy chain and identification of two genomic C gamma genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
RN [4]
RX SEQUENCE OF 132-161.
RX MEDLINE=70110015; PubMed=5461106;
RA Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
RT "Sequence studies of the Fd section of the heavy chain of rabbit
RT immunoglobulin G.";
RL Biochem. J. 116:249-259(1970).
RN [5]
RX SEQUENCE OF 129-131 AND 155-322.
RA Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
RL (In) Killander J. (eds.);
RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
RL Stockholm (1967).
CC 104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15
CC MARKERS AND REF.5 THE E15 MARKER.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M16426; AAA31289.1; -.
DR PIR; A02161; GHRB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_C1.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IgC1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT VARIANT 104 104 T -> M (IN D11 MARKER).
FT VARIANT 185 185 T -> A (IN E15 MARKER).
FT CONFLICT 48 48 N -> E (IN REF. 2).
FT CONFLICT 71 71 V -> VPV (IN REF. 2).
FT CONFLICT 144 144 Q -> E (IN REF. 3 AND 4).
FT CONFLICT 173 173 N -> D (IN REF. 5).
FT CONFLICT 187 187 Q -> E (IN REF. 3 AND 5).
FT CONFLICT 201 201 N -> D (IN REF. 5).
FT CONFLICT 218 218 Q -> E (IN REF. 5).
FT CONFLICT 233 233 E -> Q (IN REF. 5).
FT CONFLICT 246 246 N -> D (IN REF. 5).
FT CONFLICT 256 256 E -> G (IN REF. 5).
FT CONFLICT 260 260 N -> D (IN REF. 5).
FT CONFLICT 266 266 N -> D (IN REF. 5).
FT CONFLICT 280 280 Y -> W (IN REF. 5).

```


OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE (DISEASE PROTEIN WIS).
 RA MEDLINE=81021548; PubMed=6774747;
 RX Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
 RT "Primary structure of human gamma 3 immunoglobulin deletion mutant:
 RT gamma 3 heavy-chain disease protein Wis.";
 RL Biochemistry 19:4304-4308(1980).
 RN [2]
 RP REVISIONS TO 12-97 OF PROTEIN WIS.
 RX MEDLINE=77118561; PubMed=402363;
 RA Michaelson T.E., Frangione B., Franklin E.C.;
 RT "Primary structure of the 'hinge' region of human IgG3. Probable
 RT quadruplication of a 15-amino acid residue basic unit.";
 RL J. Biol. Chem. 252:883-889(1977).
 RN [3]
 RP REVISIONS TO 59-289 OF PROTEIN WIS (DISEASE PROTEIN ZUC).
 RX MEDLINE=77021516; PubMed=823945;
 RA Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C.;
 RT "The amino acid sequence of 'heavy chain disease' protein ZUC.
 RT Structure of the FC fragment of immunoglobulin G3.";
 RL Biochem. Biophys. Res. Commun. 71:907-914(1976).
 RN [4]
 RP SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).
 RX MEDLINE=82247835; PubMed=6808505;
 RA Alexander A., Steinmetz M., Barritault D., Frangione B.,
 RA Franklin E.C., Hood L., Ruxbaum J.N.;
 RT "Gamma heavy chain disease in man: cDNA sequence supports partial
 RT gene deletion model.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).
 CC -1- SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA
 CC INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11
 CC NORMALLY PRESENT IN THE HINGE REGION.
 CC -1- MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN.
 CC -1- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
 CC REF.2.
 CC -1- MISCELLANEOUS: DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION
 CC AND ALL OF THE CH1 REGION.
 CC -1- MISCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL
 CC OF THE CH1 REGION, AND PART OF THE HINGE COMPARED WITH NORMAL
 CC GAMMA-3 HEAVY CHAINS.
 CC -1- MISCELLANEOUS: DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FORM
 CC OR ANOTHER GAMMA CHAIN SUBCLASS.
 CC -1- MISCELLANEOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR
 CC TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE
 CC IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE
 CC SEGMENT (12-28).
 CC -----
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 CC -----
 CC EMBL: J00231; AAA52805.1; ALT_SEQ.
 CC PIR: A02149; G3HUI.
 CC MIM: 147120;
 CC InterPro: IPR003006; Ig_MHC.
 CC InterPro: IPR003597; Ig_c1.
 CC InterPro: IPR003600; Ig_like.
 CC Pfam: PF00047; Ig; 2.
 CC SMART: SM00407; IgC1; 1.
 CC SMART: SM00410; Ig_like; 1.
 CC PROSITE: PS00290; IG_MHC; 1.
 CC Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
 FT DOMAIN 12 73 HINGE.
 FT DOMAIN 74 183 CH2.
 FT DOMAIN 184 289 CH3.

FT REPEAT 29 43
 FT REPEAT 44 58
 FT REPEAT 59 73
 FT MOD_RES 1 1
 FT CARBOHYD 6 6
 FT DISULFID 7 7
 FT DISULFID 24 24
 FT DISULFID 27 27
 FT DISULFID 33 33
 FT DISULFID 39 39
 FT DISULFID 42 42
 FT DISULFID 48 48
 FT DISULFID 54 54
 FT DISULFID 57 57
 FT DISULFID 63 63
 FT DISULFID 69 69
 FT DISULFID 72 72
 FT CARBOHYD 140 140
 FT MOD_RES 290 290
 FT VARIANT 126 127
 FT VARIANT 134 134
 FT VARIANT 139 139
 FT VARIANT 182 182
 FT VARIANT 227 227
 FT VARIANT 227 227
 FT VARIANT 279 279
 FT SEQUENCE 290 AA; 32331 MW; E69CBC95705B2F46 CRC64;
 Query Match 46.2%; Score 1162; DB 1; Length 290;
 Best Local Similarity 91.4%; Pred. No. 6.4e-73;
 Matches 212; Conservative 11; Mismatches 9; Indels 0; Gaps 0;
 QY 239 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 298
 DB 59 EPKSCDPPPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 118
 QY 299 NWYVDGVEVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 358
 DB 119 KNYVDGVQVHNATKPREQYQNFSTFRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 178
 QY 359 ISKAKQPREPQVYTLPPSREEMTKNQVSLTCLVKGYGSPIDIAVWESNGQPENNYKTPP 418
 DB 179 ISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGYGSPIDIAVWESNGQPENNYKTPP 238
 QY 419 PVLDSGSRFLYSLKLTVDKSRWQQGNVFCGSMVEALHNHYTOKLSLSPGK 470
 DB 239 PMLDSGSRFLYSLKLTVDKSRWQQGNVFCGSMVEALHNHYTOKLSLSPGK 290
 RESULT 7
 GCL_RAT
 ID GCL_RAT STANDARD; PRT; 326 AA.
 AC P20759;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG GAMMA-1 CHAIN C REGION.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89232738; PubMed=3149946;
 RA Brueggemann M.;

RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family."
RL Gene 74:473-482(1988).

DR PIR: PS0017; PS0017.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_C1.
DR Pfam: PF00047; Ig; 3.
DR SMART: SM00407; IGcl; 2.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 112 HINGE.
FT DOMAIN 113 219 CH2.
FT DOMAIN 220 326 CH3.
FT DISULFID 27 82
FT DISULFID 102 102
FT DISULFID 106 106
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 140 200 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 246 304
FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 326 AA; 35946 MW; 013BAB45EF49B9DA CRC64;

Query Match 45.98; Score 1155; DB 1; Length 326;
Best Local Similarity 63.4%; Pred. No. 2.3e-72;
Matches 211; Conservative 52; Mismatches 60; Indels 10; Gaps 4;

QY 141 ASTRGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVHTFPAVLQSS 200
DB 1 AETAPSVPLAPGTALKSNMVLGCLVKGYFPEPTVWNSGALSGVHTFPAVLQ-S 59
QY 201 GLYSLSVTVTPSSSLGRTYICNVNHPKNTKVDKRPKSCDKTHPCPCPAPELIGG 260
DB 60 GLYTLTSSVTPSSWPSQVTCNVAHPASSTKVDKIVPRNCG--GDCKPC----ICIG 113
QY 261 ---PSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEKVNWYDGVVEVINAKTKPRE 317
DB 114 SEVSVVTFPPPKPKDVLITLTPKVTCTVVDVSHEDPEKVNWYDGVVEVINAKTKPRE 173
QY 318 QYNSTYRVSVLTVLHODWLNKGEYCKVKNKALPAPLPIETISKAKGPQRPQVYTLPPS 377
DB 174 QFNSTFRSVSELPILHODWLNKGRFCKVTSAAPSPSEKTIKPEGTQVPHVYTMGPT 233
QY 378 REEMTKNOVSLTCLVKGYFSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSLKLTVDK 437
DB 234 KEEMTQNEVSTCMVKGYPFDIVVQWQMGQPNQENYKNTPTMDTQGSYFLYSLKLVKK 293
QY 438 SRWQGNVFCSCVMHEALHNHYTKQSLSPGK 470
DB 294 EKWOQGNFTCTSVLHEGLHNHHTKSLSPGK 326

RESULT 8
GC3_MOUSE STANDARD; PRT; 329 AA.
AC P22436;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE IG GAMMA-3 CHAIN C REGION, SECRETED FORM.

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene".
RL EMBO J. 3:2041-2046(1984).

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CC -----
CC EMBL; J00451; -; NOT_ANNOTATED_CDS.
DR PIR: B02156; G3MSC.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_C1.
DR InterPro: IPR003600; Ig_Like.
DR Pfam: PF00047; Ig; 3.
DR SMART: SM00407; IGcl; 2.
DR SMART: SM00410; IG_Like; 1.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
SQ SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;

Query Match 45.7%; Score 1150; DB 1; Length 329;
Best Local Similarity 65.0%; Pred. No. 5e-72;
Matches 215; Conservative 44; Mismatches 68; Indels 4; Gaps 3;

QY 142 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVHTFPAVLQSSG 201
DB 1 TTAPSVPLVPGCDSTSGSVTLGCLVKGYFPEPTVKNVYALSSGVRTVSSVLQ-SG 59
QY 202 LYSLSVTVTPSSSLGRTYICNVNHPKNTKVDKRPKSCDKTHPC--PCPAPELIG 259
DB 60 FYSLSLTVTPSSWPSQVTCNVAHPASKTELIRIPEPR-IPKPSPPGSSCPGNIIG 118
QY 260 GPSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEKVNWYDGVVEVINAKTKPREQY 319
DB 119 GPSVFIFPKPKDALMISLTPEVTCVVDVSHEDPEKVNWYDGVVEVINAKTKPREQY 178
QY 320 NSTYRVSVLTVLHODWLNKGEYCKVKNKALPAPLPIETISKAKGPQRPQVYTLPPSP 379
DB 179 NSTFRVSVLPIHQDWMRGKEFKCKVKNKALPAPLPIETISKAKGPQRPQVYTLPPSP 238
QY 380 EMTKNQVSLTCLVKGYFSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSLKLTVDKSR 439
DB 239 QMSKKKVSILTCLVTNFFSEASVEMERNGELEQDYKNTPTPILDSDGTFLYSLKLTVDTS 298
QY 440 WOQGNVFCSCVMHEALHNHYTKQSLSPGK 470
DB 299 WLQGEIFCTSVVHEALHNHHTKQSLSPGK 329

RESULT 9
GCL_MOUSE STANDARD; PRT; 324 AA.
ID GCL_MOUSE
AC P01868;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE IG GAMMA-1 CHAIN C REGION.

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80045036; PubMed=115593;
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,

RA Takahashi N., Mano Y.;

RT "Cloning and complete nucleotide sequence of mouse immunoglobulin

gamma 1 chain gene.;"

Cell 18:559-568(1979).

[2]

RA MEDLINE=80202559; PubMed=6769752;

RP MEDLINE=80202559; PubMed=6769752; (MYELOMA PROTEIN MOPC 31C).

RA Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,

Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;

RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences

cloned in a bacterial plasmid.;"

Gene 9:87-97(1980).

[3]

RA MEDLINE=70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).

RP MEDLINE=80012837; PubMed=113776;

RA Rogers J., Clarke P., Salser W.;

RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin

heavy chain.;"

Nucleic Acids Res. 6:3305-3321(1979).

[4]

RA MEDLINE=78242288; PubMed=98524;

RP MEDLINE=78242288; PubMed=98524;

RA Adetugbo K.;

RT "Evolution of immunoglobulin subclasses. Primary structure of a

murine myeloma gammal chain.;"

J. Biol. Chem. 253:6068-6075(1978).

[5]

RA MEDLINE=73008889; PubMed=5073237;

RP MEDLINE=73008889; PubMed=5073237;

RA Swasti J., Milstein C.;

RT "The disulphide bridges of a mouse immunoglobulin G1 protein.;"

Biochem. J. 126:837-850(1972).

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DR EMBL; V00793; CAA24172.1; -

DR EMBL; V00793; CAA24173.1; -

DR EMBL; V00793; CAA24174.1; -

DR EMBL; V00793; CAA24175.1; -

DR EMBL; V00795; CAA24176.1; -

DR PIR; A02159; GIMS.

DR GlycoSuiteDB; P01868; -

DR MGD; MGI:96446; Igh-4.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003597; Ig-cl.

DR Pfam; PF00047; Ig; 3.

DR SMART; SM00407; Igcl; 2.

DR PROSITE; PS00290; IG_MHC; 1.

IMMUNOGLOBULIN DOMAIN; IMMUNOGLOBULIN C REGION; GLYCOPROTEIN;

Alternative splicing.

FT NON_TER 1 1

FT DOMAIN 1 97 CH1.

FT DOMAIN 98 110 HINGE.

FT DOMAIN 111 217 CH2.

FT DOMAIN 218 324 CH3.

FT DISULFID 27 82

FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).

FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 138 198

FT CARBOHYD 174 174 N-LINKED (GLCNAC. .).

FT /FTID-CAR_000055.

FT 244 302

FT DISULFID 324 324 REMOVED POST-TRANSLATIONALLY.

FT MOD_RES 276 276 N -> D (IN REF. 3).

FT CONFLICT 278 278 N -> D (IN REF. 3).

SQ SEQUENCE 324 AA; 35704 MW; A338812F3D1F2C93 CRC64;

Query Match 45.5%; Score 1145; DB 1; Length 324;

Best Local Similarity 62.3%; Pred. No. 1.1e-71;

Matches 207; Conservative 55; Mismatches 60; Indels 10; Gaps 4;

QY 141 ASTKGPSVFFPLAPSSKSTSGGTAALGCLVKDYFPEPTVWNSGALTSGVHTFPAVLQSS 200

Db 1 AKTTPPSVYPLAPGSAATNSMTVLGCLVKGYRPEPTVTWNSGSLSSGVHTFPAVLQSD 60

QY 201 GLYSLSVWTVPSSSLGTQYICNVNHNKPSNTKVDKRVKPEKSCDKTHTCTCP--CPAPELL 258

Db 61 -LYTSSSVTPSPSPSETVTCNVHPASSTKVDKXIVPRDCG---CRPCICTVPEV- 114

QY 259 GGSVFLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVFNNAKTKPREEQ 318

Db 115 --SSVFIFFPKPKDVLITLTPKVTCTVVDVLSKDDPEVQFSWFVDVVEVHTAQTPREEQ 172

QY 319 YNSTYRVSVTLVHODWLNKKEYCKKSVNKPALPAPIEKTISKAKGQRPFPQVYTLPPSR 378

Db 173 FNSFERSVSELPIMHODWLNKGEKFCRVNSAARPAPIEKTISKTKGRKAPQVYTIPTPK 232

QY 379 EEMTKNOVSITCLVKGYPSDIAEVESNGQPNENNYKTPPVLDSDGSFFLYSKLTVDKS 438

Db 233 EQMAKDKVSLTCTITDFPEDITVEMQWNGQPAENYKNTQPIIMNTNGSYFYVSKLNVQKS 292

QY 439 RWOQGNVFCGVMHEALHNHYTKOKLSLSPGK 470

Db 293 NWEAGNTFTCSVLHEGLHNHTKSLSHSPGK 324

RESULT 10

GC_B_RAT STANDARD; PRT; 333 AA.

ID GCB_RAT

AC P20761;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG GAMMA-2B CHAIN C REGION.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=89232738; PubMed=3149946;

RA Brueggemann M.;

RT "Evolution of the rat immunoglobulin gamma heavy chain gene family.;"

RL Gene 74:473-482(1988).

DR PIR; PS0018; PS0018.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003597; Ig-cl.

DR InterPro; IPR003600; Ig-like.

DR Pfam; PF00047; Ig; 3.

DR SMART; SM00407; Igcl; 2.

DR PROSITE; PS00290; IG_MHC; 1.

IMMUNOGLOBULIN DOMAIN; IMMUNOGLOBULIN C REGION.

FT NON_TER 1 1

FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).

FT DISULFID 27 80

FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 147 207

FT DISULFID 253 311

SQ SEQUENCE 333 AA; 36497 MW; 55F8B64D48D460A6 CRC64;

Query Match 45.5%; Score 1144.5; DB 1; Length 333;

Best Local Similarity 63.7%; Pred. No. 1.2e-71;


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CC EMBL; V00798; CAA24178.1; -
DR PIR; A02152; G2MSA.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; Igel; 2.
DR SMART; SM00410; Ig_like; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT MOD_RES 330 330 REMOVED POST-TRANSLATIONALLY.
FT SEQUENCE 330 AA; 36389 MW; B84361C5445A6864 CRC64;

Query Match 44.9%; Score 1129; DB 1; Length 330;
Best Local Similarity 63.9%; Pred. No. 1.4e-70;
Matches 212; Conservative 43; Mismatches 73; Indels 4; Gaps 3;

Qy 141 ASTKGPSVFEPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSD 200
Db 1 AKTAPSVYPLAPVCGDVTGSSVTLGCLVKGVFPPEVTLTWNSSGLSSGVHTFPAVLQSD 60

Qy 201 GLYSLSVVTPSSSLGTQTYICNVNHNKPSNTKYDKRVEPKSCDTHTCPP--CPAPEL 258
Db 61 -LYTSSSVTPSSWSPQSTCNVAHPASSTKVDKKEPRG-PTIKPCPPCKCPAPNLL 118

Qy 259 GGPVSFELPPPKDPTLMSRPEVTCVVVDVSHEDPEVKFNWYGVGVHNAKTPREEQ 318
Db 119 GGPVSFELPPPKDPTLMSRPEVTCVVVDVSHEDPEVKFNWYGVGVHNAKTPREEQ 178

Qy 319 YNSTYRVVSVTLVHQLDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYPLPPSR 378
Db 179 YNSTLRVVSALPIQHQQWMSGKEFKCKVNNKDLPAPIERTISKPKGSRAPQVYVLPPE 238

Qy 379 EEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSLKTVDKS 438
Db 239 EEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSLKTVDKS 298

Qy 439 RWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470
Db 299 NWVERNSYSCSVVHGLNHNHTTKSFSRTPGK 330

RESULT 14
GCC_RAT GCC_RAT STANDARD; PRT; 329 AA.
AC P20762;
DT 01-FEB-1991 (Rel. 17, Created)
DE 01-FEB-1991 (Rel. 17, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG GAMMA-2C CHAIN C REGION.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RX MEDLINE=8816903; PubMed=3127222;
RA Brueggemann M., Delmasiro-Galfrè P., Waldmann H., Calabi F.;
RT "Sequence of a rat immunoglobulin gamma 2c heavy chain constant
RL Eur. J. Immunol. 18:317-319(1988).
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CC -----
DR EMBL; X07189; CAA30169.1; -
DR PIR; S00847; S00847.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; Igel; 2.
DR SMART; SM00410; Ig_like; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DISULFID 15 15 CH1.
FT DISULFID 27 82 HINGE.
FT DISULFID 111 111 CH2.
FT DISULFID 113 113 CH3.
FT DISULFID 143 203 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 249 307 INTERCHAIN (WITH A HEAVY CHAIN).
FT SEQUENCE 329 AA; 36571 MW; 5FCD7B7933850773 CRC64;

Query Match 44.8%; Score 1127.5; DB 1; Length 329;
Best Local Similarity 62.8%; Pred. No. 1.8e-70;
Matches 209; Conservative 51; Mismatches 66; Indels 7; Gaps 3;

Qy 141 ASTKGPSVFEPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 200
Db 1 AKTAPSVYPLVPGSGTSGSLVTLGCLVKGVFPPEVTVKNSGALSSGVHTFPAVLQ-S 59

Qy 201 GLYSLSVVTPSSSLGTQTYICNVNHNKPSNTKYDKRVEPKSCDTHTCPP--CPAPEL 257
Db 60 GLYLTSSSVTPSSWSPQSTCNVAHPATKSNLIKRIEPR--RPKPRPTDICSDDN 116

Qy 258 LGGPSVFLPPPKDPTLMSRPEVTCVVVDVSHEDPEVKFNWYGVGVHNAKTPREE 317
Db 117 LGGPSVFLPPPKDPTLMSRPEVTCVVVDVSHEDPEVKFNWYGVGVHNAKTPREE 176

Qy 318 QYNSTYRVVSVTLVHQLDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYPLPPS 377
Db 177 QUNGTFRVYSTLHQLDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYPLPPS 236

Qy 378 REEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSLKTVDK 437
Db 237 REQMSKNKVSLSVTSMYTFYSPASISVEWERNGELEQDYKNTLPVLDSDGSFFLYSLKTVDK 296

Qy 438 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470
Db 297 DSWMRGDIYTCVSVHGLNHNHTTKSFSRTPGK 329

RESULT 15
GCC_MOUSE GCC_MOUSE STANDARD; PRT; 335 AA.
AC P01864;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG GAMMA-2A CHAIN C REGION, B ALLELE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

```

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=82037861; PubMed=6170065;
RA Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
RT "Multiple differences between the nucleic acid sequences of the
IG2a and Ig2ab alleles of the mouse.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
RN [2]
RP SEQUENCE.
RX MEDLINE=82037777; PubMed=6794027;
RA Dognin M.J., Lauwereys M., Strosberg A.D.;
RT "Multiple amino acid substitutions between murine gamma 2a heavy
chain fc regions of Ig1a and Ig1b allotypic forms.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
CC -1- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
CC FROM BALB/C MICE, AT 15% OF THE POSITIONS.
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CC -----
CC EMBL; J00479; ; NOT_ANNOTATED_CDS.
DR PIR; A02153; G2MSAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IGc1; 2.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
SQ SEQUENCE 335 AA; 36596 MW; FA3382792CBB13C6 CRC64;

Query Match 44.8%; Score 1126.5; DB 1; Length 335;
Best Local Similarity 61.6%; Pred. No. 2.1e-70;
Matches 207; Conservative 52; Mismatches 70; Indels 7; Gaps 2;

QY 141 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
Db 1 AKTTAPSVYPLVPVCGGTGSSVTLGCLVKGYRPEPTLTWNSGSLSSGVHTFPAVLQ-S 59
QY 201 GLYSLSSVTVTPSSSLGTQYIYICNVNHPKNTKVKRVEPK-----SCDKTHTCPPCPA 254
Db 60 GLYTLSSSVTVTSNTWPSQTITCNVAHPASSTKVDKKIEPRVPTQNCPHPHORVPPECA 119
QY 255 PELLGGPSVFLEPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDDGVVHNATKP 314
Db 120 PDLGGPSVFIFPPKIKDVLMSISLSPVTCVVVDSEDDPDVQVLSFVNVEVHTAQQT 179
QY 315 REEQYNSTYRWVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTIISKAKGPREPQVYTL 374
Db 180 HREDYNSTLRVVSALPIQHODWMSGKEFKCKVNNRALSPIEKTIISKPGVRAQVYVL 239
QY 375 PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPTPVLDSGSEFLYSKLT 434
Db 240 PPAEEMTKKEFSLTCLMITGFLPAETAVDWTNSGRTEQYKNTATVLDSGSEFLYSKLR 299
QY 435 VDKSRWOGNVFSCSVNMEALHNYTKLSLSLSPGK 470
Db 300 VQKSTWERSGLFACSVVHEVLHNLHTTKTISRSLGK 335

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OM protein - protein search, using sw model

Run on: April 17, 2002, 16:40:41 ; Search time 40.91 Seconds
(without alignments)
1680.469 Million cell updates/sec

Title: US-09-499-662-117
Perfect score: 2517
Sequence: 1 MGWSCILFLVATATGVHSQ.....MHEALHHYTKSLSPGK 470

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL17:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mbc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1636.5	65.0	473	11	Q9D8L4	Q9d8l4 mus musculus
2	1625.5	64.6	463	11	Q99LC4	Q99lc4 mus musculus
3	1585.5	63.0	473	11	Q99L25	Q99l25 mus musculus
4	1559	61.9	468	11	Q99L31	Q99l31 mus musculus
5	1433.5	57.0	437	11	Q9RIA4	Q9ria4 mus musculus
6	859	34.1	500	4	Q9BRV0	Q9brv0 homo sapien
7	759.5	30.2	597	4	Q9BU10	Q9bu10 homo sapien
8	755.5	30.0	597	4	Q9BQ88	Q9bq88 homo sapien
9	755	30.0	484	11	Q99LA6	Q99la6 mus musculus
10	721.5	28.7	487	11	Q99KA4	Q99ka4 mus musculus
11	649	25.8	479	11	Q99M22	Q99m22 mus musculus
12	602	23.9	426	11	Q9DCD9	Q9dcd9 mus musculus
13	577.5	22.9	416	4	Q9NPP6	Q9npp6 homo sapien
14	522	20.7	150	4	Q9Y298	Q9y298 homo sapien
15	505	20.1	157	4	Q95978	Q95978 homo sapien
16	480.5	19.1	384	4	Q9UP60	Q9up60 homo sapien
17	466	18.5	119	4	Q9UL94	Q9ul94 homo sapien
18	465.5	18.5	124	4	Q9UL92	Q9ul92 homo sapien
19	455	18.1	117	11	Q9QXF0	Q9qxf0 mus musculus

20	454	18.0	119	5	Q9QYZ2	Q9qyz2 schistosoma
21	452	18.0	125	4	Q9UL95	Q9ul95 homo sapien
22	445.5	17.7	116	4	Q9UL89	Q9ul89 homo sapien
23	441.5	17.5	118	11	Q9Z1C4	Q9z1c4 mus musculus
24	439	17.4	117	11	Q9QXE9	Q9qxe9 mus musculus
25	437.5	17.4	114	11	Q9JL81	Q9jl81 mus musculus
26	436.5	17.3	147	4	Q9Y509	Q9y509 homo sapien
27	433.5	17.2	110	11	Q9JL77	Q9jl77 mus musculus
28	417	16.6	111	11	Q9D988	Q9d988 mus musculus
29	415.5	16.5	109	11	Q9JL75	Q9jl75 mus musculus
30	400	15.9	117	11	Q9Z1C6	Q9z1c6 mus musculus
31	399	15.9	375	4	Q9BS21	Q9bs21 homo sapien
32	393	15.6	684	13	Q90544	Q90544 ginglymosto
33	385.5	15.3	110	11	Q9JL83	Q9jl83 mus musculus
34	371.5	14.8	298	11	Q9QYF0	Q9qyf0 mus musculus
35	357	14.2	120	4	Q9BUA1	Q9bua1 homo sapien
36	356	14.1	109	11	Q9JL85	Q9jl85 mus musculus
37	333	13.2	113	4	Q9UL90	Q9ul90 homo sapien
38	324	12.9	121	4	Q9UL71	Q9ul71 homo sapien
39	323.5	12.9	118	4	Q9UL91	Q9ul91 homo sapien
40	323	12.8	131	4	Q9UL88	Q9ul88 homo sapien
41	320.5	12.7	112	4	Q9HCC1	Q9hcc1 homo sapien
42	315.5	12.5	122	4	Q9UL84	Q9ul84 homo sapien
43	314	12.5	116	4	Q9UL93	Q9ul93 homo sapien
44	306.5	12.2	118	4	Q9UL72	Q9ul72 homo sapien
45	302.5	12.0	150	4	Q95973	Q95973 homo sapien

ALIGNMENTS

RESULT	1
Q9D8L4	
ID	Q9D8L4
AC	Q9D8L4; PRELIMINARY; PRT; 473 AA.
DT	01-JUN-2001 (Tremblrel. 17, Created)
DT	01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT	01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE	1810060009RIK PROTEIN.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX	MEDLINE=21085660; PubMed=11217851;
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Yoshino M., Itoh M., Ishii Y.,
RA	Kawai J., Shinagawa A., Shibata K., Kiyosawa H., Kondo S., Yamanaka I.,
RA	Alzawa K., Izawa M., Nishi K., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA	Saito T., Okazaki Y., Gojobori T., Ashburner M., Batalov S., Casavant T.,
RA	Kadota K., Matsuda H.A., Gasterland T., Gissi C., King B., Kochiwa H.,
RA	Fleischmann W., Gaasterland T., Nikaido I., Pesole G., Quackenbush J.,
RA	Kuehl P., Lewis S., Stäubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA	Schriml L.M., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA	Sakai K., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Cariboldi M.,
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA	Suzuki H., Toyooka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA	Havashizaki Y.
RT	"Functional annotation of a full-length mouse cDNA collection."
RL	Nature 409:685-690(2001).
CC	-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.
DR	EMBL; AK007918; BAB25349.1; "
DR	MGI; 1924014; 1810060009RIK.
DR	InterPro; IPR003599; Ig.

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DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_4.
DR SMART; SM00409; Ig_2.
DR SMART; SM00407; Igcl; 3.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; Ig_Like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Query Match 65.0%; Score 1636.5; DB 11; Length 473;
Best Local Similarity 63.7%; Pred. No. 3.5e-124;
Matches 303; Conservative 70; Mismatches 94; Indels 9; Gaps 4;

QY 1 MGWSCIILFLVATATGVHVSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVKQAP 60
DB 1 MEWVWFLFLSVTAGVHVSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVKQAP 60
QY 61 GQGLEWGEIDPDSYTYNOKFKGKATLTVDSTSTAYMELSLRSRSEDYAVYICARNRD 120
DB 61 GQGLEWGEIDPDSYTYNOKFKGKATLTVDSTSTAYMELSLRSRSEDYAVYICARNRD 120
QY 121 YSNWYFDVWGEGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
DB 121 YSNWYFDVWGEGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
QY 122 YSDYDFAYWGGTGLTVVSAAKTTPPSVYPLAPSGAQTQNTYICNVNKKPSNTKVDKRVPE 179
DB 122 YSDYDFAYWGGTGLTVVSAAKTTPPSVYPLAPSGAQTQNTYICNVNKKPSNTKVDKRVPE 179
QY 181 WNSGALTSQVHTFPVAVLQSGSLYSLSVTVVPSSSLTQTYICNVNKKPSNTKVDKRVPE 240
DB 181 WNSGALTSQVHTFPVAVLQSGSLYSLSVTVVPSSSLTQTYICNVNKKPSNTKVDKRVPE 240
QY 241 KSCDKTHTCPP--CPAPELGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 298
DB 241 KSCDKTHTCPP--CPAPELGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 298
QY 299 NWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLDHQLNGKEVCKVSNKALPAPIEKT 358
DB 299 NWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLDHQLNGKEVCKVSNKALPAPIEKT 358
QY 359 ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 418
DB 359 ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 418
QY 419 PVLDSGDSFELYSLKLTVDKSRWQGNVFCFVSMHEALHNHYTQKSLSLSPGK 470
DB 419 PVLDSGDSFELYSLKLTVDKSRWQGNVFCFVSMHEALHNHYTQKSLSLSPGK 470
QY 421 PIMTDGSGYFIYSLKLVQKSNWEAGNTFTCSVLHEGLHHNHTKSLSHSPGK 463
DB 421 PIMTDGSGYFIYSLKLVQKSNWEAGNTFTCSVLHEGLHHNHTKSLSHSPGK 463

RESULT 3
Q99L25 PRELIMINARY; PRT; 473 AA.
AC Q99L25;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCBI_TaxID=10090;
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003888; AAH03888.1; -.
SQ SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;

Query Match 63.0%; Score 1585.5; DB 11; Length 473;
Best Local Similarity 63.4%; Pred. No. 4.7e-120;
Matches 301; Conservative 61; Mismatches 106; Indels 7; Gaps 5;

QY 1 MGWSCIILFLVATATGVHVSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVKQAP 60
DB 1 MEWVWFLFLSVTAGVHVSQVQLVQSGAEVKKPGASVKVSCKASGYTFTDTHIHWVKQAP 60
QY 61 GQGLEWGEIDPDSYTYNOKFKGKATLTVDSTSTAYMELSLRSRSEDYAVYICARNRD 120
DB 61 EGGLEWIGYIVPRDGSYTYNOKFKGKATLTADKSSSTAYMQLNSLTSEDSAVCFCSRGS 120
QY 121 --YSNN--WYFDVWGEGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV 177
DB 121 IYGYGLYFDYWGQGTITVSSAKTTPPSVYPLAPSGAQTQNTYICNVNKKPSNTKVDKRV 180
QY 178 TVSNWNSGALTSQVHTFPVAVLQSGSLYSLSVTVVPSSSLTQTYICNVNKKPSNTKVDKRV 237
DB 181 TLWNNSGSLSGVHTFPVAVLQSD--LYTLSSSVTVVTSSTSSQSLTCNVNAPASSTKVDKK 239
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DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_4.
DR SMART; SM00409; Ig_2.
DR SMART; SM00407; Igcl; 3.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; Ig_Like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Query Match 65.0%; Score 1636.5; DB 11; Length 473;
Best Local Similarity 63.7%; Pred. No. 3.5e-124;
Matches 303; Conservative 70; Mismatches 94; Indels 9; Gaps 4;

QY 1 MGWSCIILFLVATATGVHVSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVKQAP 60
DB 1 MEWVWFLFLSVTAGVHVSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVKQAP 60
QY 61 GQGLEWGEIDPDSYTYNOKFKGKATLTVDSTSTAYMELSLRSRSEDYAVYICARNRD 120
DB 61 GQGLEWGEIDPDSYTYNOKFKGKATLTVDSTSTAYMELSLRSRSEDYAVYICARNRD 120
QY 121 YSNWYFDVWGEGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
DB 121 YSNWYFDVWGEGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
QY 122 YSDYDFAYWGGTGLTVVSAAKTTPPSVYPLAPSGAQTQNTYICNVNKKPSNTKVDKRVPE 179
DB 122 YSDYDFAYWGGTGLTVVSAAKTTPPSVYPLAPSGAQTQNTYICNVNKKPSNTKVDKRVPE 179
QY 181 WNSGALTSQVHTFPVAVLQSGSLYSLSVTVVPSSSLTQTYICNVNKKPSNTKVDKRVPE 240
DB 181 WNSGALTSQVHTFPVAVLQSGSLYSLSVTVVPSSSLTQTYICNVNKKPSNTKVDKRVPE 240
QY 241 KSCDKTHTCPP--CPAPELGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 298
DB 241 KSCDKTHTCPP--CPAPELGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 298
QY 299 NWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLDHQLNGKEVCKVSNKALPAPIEKT 358
DB 299 NWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLDHQLNGKEVCKVSNKALPAPIEKT 358
QY 359 ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 418
DB 359 ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 418
QY 419 PVLDSGDSFELYSLKLTVDKSRWQGNVFCFVSMHEALHNHYTQKSLSLSPGK 470
DB 419 PVLDSGDSFELYSLKLTVDKSRWQGNVFCFVSMHEALHNHYTQKSLSLSPGK 470
QY 421 PIMTDGSGYFIYSLKLVQKSNWEAGNTFTCSVLHEGLHHNHTKSLSHSPGK 463
DB 421 PIMTDGSGYFIYSLKLVQKSNWEAGNTFTCSVLHEGLHHNHTKSLSHSPGK 463

RESULT 2
Q99LC4 PRELIMINARY; PRT; 463 AA.
AC Q99LC4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCBI_TaxID=10090;
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003435; AAH03435.1; -.
SQ SEQUENCE 463 AA; 51007 MW; BAA674C6BBBC30783 CRC64;

Query Match 64.6%; Score 1625.5; DB 11; Length 463;
Best Local Similarity 63.6%; Pred. No. 2.7e-123;
Matches 300; Conservative 72; Mismatches 89; Indels 11; Gaps 5;
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QY 238 VEPKSCDKTHTCPP--CPAPELGGPSVFLPPPKDFTLMSRTPEVTCVVVDVSHEDPE 295
Db 240 IEPGRG-PTIKPCPPCKCAPNLGGPSVFIIPPKIKDVLMSLSLSPMVTCCVVVDVSEDDPD 298
QY 296 VKFNWYDGVGVHNAKTPREQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI 355
Db 299 VOISFVNNVEVLAQTOTHRDYNSTLRVVSALPFIQHODWMSGKEFKCKVNNKALPAPI 358
QY 356 EKTISKAGGKGPQVYVLPDSRREMTKNQVSLCLVKGFGFVPSDIAVWESNGQPENNYK 415
Db 359 ERTISKPGSVRAQVYVLPDSRREMTKNQVSLCLVKGFGFVPSDIAVWESNGQPENNYK 418
QY 416 TTPPVLDSDGSFELYKLTVDKSRWQQGNVFCSCVMHEALHNHYTKLSLSPGK 470
Db 419 NTEPVLDSDGSFELYKLTVDKSRWQQGNVFCSCVMHEALHNHYTKLSLSPGK 473

RESULT 4
ID Q99L31 PRELIMINARY; PRT; 468 AA.
AC Q99L31;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
OS SIMILAR TO RIKEN CDNA 1810060009 GENE.
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003878; AA03878.1; -.
SQ SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;
```

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Query Match 61.98; Score 1559; DB 11; Length 468;
Best Local Similarity 62.79; Pred. No. 6.4e-118;
Matches 296; Conservative 62; Mismatches 108; Indels 6; Gaps 4;

QY 1 MGWSCIILFVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVKAP 60
Db 1 MKCSWIFFLNAVGVNSEVQLQSGAEVLRPGASVKLSCTASGFKLSDLMHWVKORP 60
QY 61 GQGLWMEIDPSYTYNOKFKGKATLVDTSTSTAYMELSLRSDEDTAVYYCARNRD 120
Db 61 EQGLEWIGWIDPGETKYAPKFDQKATITADTSSNTAYLQLSLTSEDYIYCARNLL 120
QY 121 YSNWYFDVWEGEGLTVTVSSASTKGPSVFPLAPSKSTSGGTAALGCLVKDYFPEPVTVS 180
Db 121 YGG--YDYWGQGGTITVSSAKTTPSYVPLAPVCGDPTGSSVTLGCLVKGFFPEPVTLT 178
QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTOTYICNVNHPKSTKVDKRVPE 240
Db 179 WNSGSLSSCVHTFPAVLQSD--LYTLSSSVTVTPSTWPSQSTCNVAHPASSTKVDKKTLEP 237
QY 241 KSCDKTHTCPP--CPAPELGGPSVFLPPPKDFTLMSRTPEVTCVVVDVSHEDPEVKF 298
Db 238 RG-PTIKPCPPCKCAPNLGGPSVFIIPPKIKDVLMSLSLSPMVTCCVVVDVSEDDPDVQI 296
QY 299 NWYDGVGVHNAKTPREQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 358
Db 297 SWFNNVEVLAQTOTHRDYNSTLRVVSALPFIQHODWMSGKEFKCKVNNKALPAPIERT 356
QY 359 ISKAGGKGPQVYVLPDSRREMTKNQVSLCLVKGFGFVPSDIAVWESNGQPENNYKTP 418
Db 357 ISKPGSVRAQVYVLPDSRREMTKNQVSLCLVKGFGFVPSDIAVWESNGQPENNYKTE 416
QY 419 PVLDSDGSFELYKLTVDKSRWQQGNVFCSCVMHEALHNHYTKLSLSPGK 470
Db 417 PVLDSDGSFELYKLTVDKSRWQQGNVFCSCVMHEALHNHYTKLSLSPGK 468
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RESULT 5
Q99IA4
ID Q99IA4 PRELIMINARY; PRT; 437 AA.
AC Q99IA4;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE GAMMAL HEAVY CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G.; Yu X.; Ekramoddoullah A.K.M.; Misra S.;
RL "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF152372; AAD40243.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_Like; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 437
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;
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Query Match 57.08; Score 1433.5; DB 11; Length 437;
Best Local Similarity 59.18; Pred. No. 8.1e-108;
Matches 267; Conservative 72; Mismatches 96; Indels 17; Gaps 7;

QY 21 VOLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVKAPGQGLWMEIDPSDYTYN 80
Db 1 VOLQESGGLVKKPGSGLKLSCAASGFTSSYAMSVRQTPEKRLWVASFS--SGGIYYT 59
QY 81 QKFKGKATLVDTSTSTAYMELSLRSDEDTAVYYCARNRDYNNWYFDVWEGEGLTVTVSS 140
Db 60 DSVKGRFTIYKDKRNILSLQMSLSRSEDYAMYCARG--DYS----AYWGPGLTVTVA 113
QY 141 ASTKGPSVFPLAPSKSTSGGTAALGCLVKDYFPEPVTVSNWNSGALTSGVHTFPAVLQSS 200
Db 114 AKTTPSYVPLAPGSAQAQNSMVTLGCLVKGFFPEPVTVSNWNSGALTSGVHTFPAVLQSD 173
QY 201 GLYSLSSVTVTPSSSLGTOTYICNVNHPKSTKVDKRVPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTPRE 258
Db 174 -LYTLSSSVTVTPSTWPSQSTCNVAHPASSTKVDKKTIVPRDCG---CKPICITVPEV- 227
QY 259 GGPSVFLPPPKDFTLMSRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTPRE 318
Db 228 --SSVFIFPPKPKDVLTLTPKVKTCVVVDISKDDPEVQFSWFVDVDEVHTAQTQPREQ 285
QY 319 YNSIYRVVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAGGKGPQVYVLPDSR 378
Db 286 FNSTFRSVELPMHQDWLNGKEFKCRVNSAFAFPAPIEKTISKTRKRPAPQVYVTPPK 345
QY 379 EEMTKNOVSLCLVKGFGFVPSDIAVWESNGQPENNYKTPPVLDSDGSFELYKLTVDK 438
Db 346 EQMAKDKVSLCTMTDFPEDITVWQNGQPAENYKNTQPIMDTDGTFVTSKUNVOKS 405
QY 439 RWQGNVFCSCVMHEALHNHYTKLSLSPGK 470
Db 406 NWEAGNTFTCSVLHHEGLHNHHTKLSLSPGK 437
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RESULT 6
Q9BRV0 PRELIMINARY; PRT; 500 AA.
AC Q9BRV0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:14588).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005951; AA05951.1; -.
SQ SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;

Query Match 34.1%; Score 859; DB 4; Length 500;
Best Local Similarity 41.1%; Pred. No. 2.6e-61;
Matches 206; Conservative 68; Mismatches 177; Indels 50; Gaps 18;

QY 1 MGWSCIILFLVATGATGHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVQKAP 60
Db 1 MDWTWISILFLVAAATGAQSQVHLVQSGAEVMSPGASVRVSKTGYAFHTYSIIWVQAP 60
QY 61 GQGLEWGEIDPSDSTYNQKFKGKATLVDTSTSTAYMELSLRSEDATVYICARNR- 119
Db 61 GQGLEWGWISPSDNTFRFAKFGQVTLTDTSTSYMELSLRSDATVYICARRYC 120
QY 120 DYS---NNWYF---DVMGEGTLTVSSASTKGPSVFPPLAPSSKSTSGTAALGCLVKDYF 173
Db 121 SYSSCONDYIIYMDVWGKGTITVSSASPTSPKVPFLSLS-TQPGNVVIACLVGQFF 179
QY 174 P-EPVTVSWNSGALTSGVHTFPAVLQSSG-LYSLSSVTVTPSSS-LGTQTYICNVNHNKPS 230
Db 180 PQEPLSVTWSESQGVVARNFPSPQDASGDLYTSSQLTLPATQCLAGKSVTCHKVHY-T 238
QY 231 NTKVDKREPKSKDTHTCPAPPELLGGPSVFLFPPKPK-----DTLM 275
Db 239 NPSQDVTV-----PCVPSPPTPTSPST-PPTPSPSCCHPRLSLHRPALEDLL 285
QY 276 ISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREQYNSTYRVVSVLTVHQD 335
Db 286 LGSEANLTCLTGL-RDASGVTFWTWTPSSGK--SAVQGPDPDRDLCGCYSVSSVLSCGAEP 342
QY 336 WLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ-VSLTCLVKG 394
Db 343 WNHGKTFCTAAVPESTKPLTATLSKS-GNTRFPEVHLLPPPSSEALNELVTLTCLARG 401
QY 395 FYPSDIAVWESNQ--PENNYKTPPVLD-SDG--SFFLYSKLTVDKSRQOQNVFSCS 449
Db 402 FSPKDVLRVQLQSGQELPREKYLUTWASRQEPSSQGTTFVAVTSLRVAADWKMGDTFCM 461
QY 450 VMHEALHNHYTQKSLSLSPGK 470
Db 462 VGHGALPLAFTQETIDRLACK 482

RESULT 7
Q9BU10 PRELIMINARY; PRT; 597 AA.
AC Q9BU10;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE UNKNOWN (PROTEIN FOR MGC:1652).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

RESULT 8
Q9BOB8 PRELIMINARY; PRT; 597 AA.
AC Q9BOB8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:1905) (PROTEIN FOR MGC:1228).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
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```
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LYMPHOMA;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002963; AA02963.1; -.
SQ SEQUENCE 597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;

Query Match 30.2%; Score 759.5; DB 4; Length 597;
Best Local Similarity 31.4%; Pred. No. 3.6e-53;
Matches 181; Conservative 91; Mismatches 187; Indels 117; Gaps 17;

QY 8 LFLVATATGHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVQKAPQGGLEWM 67
Db 8 LLLVAAPRWLSQVQLQWAGLGLKSETLSLTCTGVGSGFYIWSVPPQKGLDWI 67
QY 68 GEIDPSDSTYNQKFKGKATLVDTSTSTAYMELSLRSEDATVYICAR-----NRDYS 122
Db 68 GEINHSGS-TNYPNLSKSRVTISVDTSKQLSLKLSLVNNAADTAVYICARVITRASPGTD 126
QY 123 NNWYFDWEGTLTVSSASTKGPSVFPPLAPSSKSTSG-GTAALGCLVKDYFPFPTVSW 181
Db 127 GRYGMDVWGQGTITVTVSSGASAPFLFPLVSCNSPDTSSVAVGCLAQDFLPDSITFSW 186
QY 182 --NSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSL--GTQTY-ICNVNHNKPSN----- 231
Db 187 KYKNSDISSTRGPSVLR-GGKYAATSQVLLPSKDVWQGTDEHVCKVQHPNGKKNV 245
QY 232 -----TKVDKRVPEKPS-----CDKTHTCP----- 250
Db 246 PLPIVIAELPKKVSFVFPDRDGFNPKRKSLLICQATGFSRQIQVSWLRGCKQVSGVTT 305
QY 251 -PCPAPELLGGPS----- 262
Db 306 DQVQAEAKESGPTTYKVTSTLTIKESDWLSQSMTFCRVDHRGLTFQONASSMCPVDQDTA 365
QY 263 --VFLFPKPKDGLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREQYN 320
Db 366 IRVFAIAPS-FASIFLTKSKLCLVLDLTIDYD-SVTISWTRQNGEAVKHTNISEHPN 423
QY 321 STYRVSVLTVLHODWLNKEYKCKVSNKALPAPIEKTISKAKGQ-REPOVYTLPPSRE 379
Db 424 ATFSAVGEASTCEDDWNSEGERFTCTVHTDLPSPKQTIISRPKGVALLHRPDVILLPPARE 483
QY 380 EMT-KNOVSLTCLVKGYFSPDSIAVWESNQGP--ENNYKTPPVLD--SDGSFFLYSKLT 434
Db 484 QLNLRSATITCLVTGFSPADVFQNMQRGQPLSPERYVTSAPMPEQAPGRYFAHSILT 543
QY 435 VDKSRWQGNVFSQSVMEALHNHYTQKSLSLSPGK 470
Db 544 VSEEWNTGETYTCVVAHEALPNRVTERTVDKSTGK 579

RESULT 9
Q9BU10 PRELIMINARY; PRT; 597 AA.
AC Q9BU10;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE UNKNOWN (PROTEIN FOR MGC:1905) (PROTEIN FOR MGC:1228).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
```



```

Db 61 EKRLEWATISDGGSYTYYPONVKGRETFISRDNAKNLNLYLQMSHLKSDTAMTYCARDWG 120
Qy 119 -ROYSNMYFDWEGTLVTVSSASTGSPVPLAPSSKTSGGTAALGCLVKDYFPE-P 176
Db 121 GSPYGGYRFYWGQGTITVSSSESARNPTIYPLT-LPRALSSDPVIGLIHDIYFSGT 179
Qy 177 VTSWNSGALTSVHTTFAVLQSSGLXSLSSVTVTPSSSLGT-QTYICNVNHRKPSNTKVD 235
Db 180 MNVTWGRSGKDTTVNPPALASGGYTMSSQLTLPAVECPGESVKSQVQH---DSNAV 236
Qy 236 KRVEPKCDKTHTCPPCAPPELLGSPSVFLFPKPKDTLMISRTPEVTCVVYVSHEDPE 295
Db 237 QELDVKCSGPPPCPCP-PSC--HPSLSLQRPALD-LLGSDASLTCTLGLNRNPEGA 292
Qy 296 VKFNWYDGVHNAKTKPREQYNST---YRVVSVLTVLHODWLNGKEYCKVSKYNALP 352
Db 293 V-FTW-----EPSTGKDAVQKAVQNSCGCYSVSVLPGCAERNWSGASFCKTTHPESD 346
Qy 353 APIEKTISKAKGQPREPVYTLPPSREEMTKNQ-VSLTCLVKGFYPSDIAVWESNGQ-- 409
Db 347 T-LRGTIAKIVNTFPQVHLLPPLPSEELALNELVSLTCLVRAFPKPEVLVRWLHNGNEEL 405
Qy 410 -PENNYKITPPVLDSG--SFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKLSLSL 466
Db 406 SPESYLVEPLKEPGEATTVLTVSVLSVSAETWKGQDQVSCMVGHEALPMNFTQKTIDR 465
Qy 467 SPGK 470
Db 466 LSGK 469

RESULT 11
Q99M22 ID Q99M22 PRELIMINARY; PRT; 479 AA.
AC Q99M22;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:6342).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staahl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:585-590(2001).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AK002875; BAB22422.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 426 AA; 45619 MW; 56E1275BA48F6FB1 CRC64;

Query Match 25.88; Score 649; DB 11; Length 479;
Best Local Similarity 33.88; Pred. No. 2.3e-44;
Matches 161; Conservative 89; Mismatches 194; Indels 32; Gaps 18;

Qy 7 ILFLVATATGVSQVLQVQSGAEVKKPKGASVKVSKAGSYFTTS-YWQWVKAPAGGLE 65
Db 6 LLYLLTAIPGLSDVQLQESGPGLVKPSQSLSLTCSTGYTSITSYWNWIRQPPGNKLE 65
Qy 66 WMGIDPSDSYTNQKFGKATLVDTSTAYMELSSLRSEDYAVYICARNRDYNNW 125
Db 66 WMGYIN-YDGSNNYNPSLKNRISITRDTSKNQFPFLKLSVTTEDATVYCA-SRGYS--- 120
Qy 126 YFDVWGEGLTVVSSATGKPSVPLAPSSKTSGGTAALGCLVKDYFPE-PVTVSWNSG 184
Db 121 WFPNWGGTLTVSSAESARNPTIYPLT-LPALSSDPVIGLIHDIYFSGTMVNTWGS 179
Qy 185 ALTSQVHTFAVLQSSGLYSLSSVTVTPSSSLGT-QTYICNVNHRKPSNTKVKRVEPKSC 243
Db 180 GKDITTVNFPALASGGRYTMSSQLTLPAVECPGESVKSQVQH-DSNPVQELDV---NC 235

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Query Match 23.9%; Score 602; DB 11; Length 426;
Best Local Similarity 32.6%; Pred. No. 1.3e-40;
Matches 157; Conservative 75; Mismatches 165; Indels 84; Gaps 16;

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Qy 244 DKHTCTPCCPAPELLGGPSVFLFPKPKDTLMISRTPEVTCVVYVSHEDPEVKNWYVD 303
Db 236 SGPTPPPIITIPSC--QPSLSLQRPALD-LLGSDASITCTLGLNRNPEGAV-FTW--- 288
Qy 304 GVEVHNAKTKPREQYNST---YRVVSVLTVLHODWLNGKEYCKVSKYNALPAPIEKTIS 360
Db 289 --EPSTGKDAVQKAVQNSCGCYSVSVLPGCAERNWSGASFCKTTHPE-SGTITGTIA 345
Qy 361 KAKGQPREPVYTLPPSREEMTKNQ-VSLTCLVKGFYPSDIAVWESNGQ---PENNYKT 416
Db 346 KVTYNTVTPVHLLPPLPSEELALNELVSLTCLVRAFPKPEVLVRWLHNGNEELSPESYL 405
Qy 417 TTPVLDSG--SFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKLSLSLSPGK 470
Db 406 EPLKEPGEATTVLTVSVLSVSAETWKGQDQVSCMVGHEALPMNFTQKTIDRLSGK 461

RESULT 12
Q9DCD9 ID Q9DCD9 PRELIMINARY; PRT; 426 AA.
AC Q9DCD9;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE ADULT MALE KIDNEY CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
DE CLONE:0610041A01, FULL INSERT SEQUENCE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staahl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:585-590(2001).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AK002875; BAB22422.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 426 AA; 45619 MW; 56E1275BA48F6FB1 CRC64;

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QY 1 MGWSCIILFLVATATGTVHVSQVQVGVKPGASVSKYSCASGVTFTSYWQWVKQAP 60
 DB 1 MFSRIFLFLSVTTC-----16
 QY 61 GOGLEWMEIDPSDSTYNNOKFKGKATLTVDTSTSTAYMELSSLSRSEDATVYYCARNRD 120
 DB 17 -----NGDTSYNOKFKGKATLTVDKSSSTAYMQLSSLTSEDSAYFFCARS-D 62
 QY 121 YSNWYFDVWGBGTLTVTSSASTKGPSPVPLAPSSKSTSGGTAALCGLVKDYFPE-PVTV 179
 DB 63 YGPTAMDYWGOGTSTVSSSARNTIYPLT-LPRALSSDPVILGCLIHDFPSGTMNV 121
 QY 180 SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGT-QTYICNVNHPKSTKVKREV 238
 DB 122 TWKSGKDTTVNFPALASGGYTWSSQLTLPVCEPGEBSVKSVQH---DSNAVQEL 178
 QY 239 EPKSCDKTHTCPPAPPELLGCGSVFVLPKPKDLMISRTEVTVVVDVSHEDPEVKF 298
 DB 179 DVKSGPPPCPCP-PS-PPSLSLQRPALD-LLLGSDASLCTLGLNRPGEAV-F 233
 QY 299 NMYVDGVEVHNATKPREQYNST---YRVSVLTVLHODWLNKGYKCKVSNKALPAPI 355
 DB 234 TW-----EPSTGKDAVOKAVQNSCGCYSVSVLPCCAEWMNSGAFKCTVTHPESDT-L 287
 QY 356 EKTISKAGQPREPOVYTLPPSREEMTKNQ-VSLTCLVKGFYPSDIAVEWESNGO---PE 411
 DB 288 TGTIAKITVNTPPQVHLLPPSEBALNELVSLTCLVAFNPKFVRLWHLGNELSP 347
 QY 412 NNYKTPPVLDSDG--SFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPG 469
 DB 348 SYLVEPLKEPEGATTVLTVSVLRSVLAELWKQGVSCMWGHEALPMNFTQKTIDRLSG 407
 QY 470 K 470
 DB 408 K 408

RESULT 13

Q9NPP6 PRELIMINARY; PRT; 416 AA.
 ID Q9NPP6
 AC Q9NPP6
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE IMMUNOGLOBULIN HEAVY CHAIN VARIANT (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pluvinet R., Estivill X., Escarceller M., Sumoy L.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Auffray C., Ansorge W., Ballabio A., Estivill X., Gibson K.,
 RA Leirach H., Poustka A., Lundeberg J.;
 RT "The European IMAGE Consortium for Integrated Molecular analysis of
 human gene transcripts."
 RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN
 DR EMBL; AL389978; CAB97534.1; -.
 DR InterPro; IPR003600; Ig_Like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 4.
 DR SMART; SM00406; Igv; 1.
 DR SMART; SM00410; Igv; 1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 FT NON_TER 1
 SQ SEQUENCE 416 AA; 44786 MW; 8C41708BB8AB4687 CRC64;

Query Match

20.7%; Score 522; DB 4; Length 150;

Query Match 22.9%; Score 577.5; DB 4; Length 416;
 Best Local Similarity 35.2%; Pred. No. 1.2e-38;
 Matches 149; Conservative 66; Mismatches 171; Indels 37; Gaps 17;
 QY 60 POGLEWMEIDPSDSTYNNOKFKGKATLTVDTSTSTAYMELSSLSRSEDATVYYCARNR 119
 DB 1 POGLEWVSRISSGDTVDYADSVKGRFTVSRDTAKNSLSLQSSLRVEDATVYYCAR-- 58
 QY 120 DYSNNWY-FDVWGBGTLTVTSSASTKGPSPVPLAPSSKSTSGGTAALCGLVKDYFPEP 177
 DB 59 -----IYIGNDVWGQGTTVTVSSASPTSPKVFPLSLDS-TPDGNVVVACLVQGFPPQ 113
 QY 178 TVSNWNGALTSGVHTFPAVLQSSG-LYSLSSVTVVPPSSSL-GTQTYICNVNHH--KFSNTK 233
 DB 114 SVTWSGQNVFARNPPPSQDASGLDLYTSSQLTLPATQCPDGKSVTCHVKHYTNP 171
 QY 234 VDKRVEPKSCDTHTCPPAPPELLGCGSVFVLPKPKDLMISRTEVTVVVDVSHED 293
 DB 172 -----DVTVPVPPPPCC-HPRLSLRPALED-LLLGSEANLTCTLTGL-RDA 218
 QY 294 PEVKFNWYVDGVEVHNATKPREQYNSTYRVSVLTVLHODWLNKGYKCKVSNKALPA 353
 DB 219 SGATETWTPSSGK--SAVQGPPELDLGGCYSVSVLPGCCAQPMNHGETFTCTAAHP 276
 QY 354 PIEKTIKAKGQPREPOVYTLPPSREEMTKNQ-VSLTCLVKGFYPSDIAVEWESNQ--P 410
 DB 277 PUTANITKS-GNTFRPEVHLLPPSEBALNELVTLTCLARGFSPKDVLRVLQSGQELP 335
 QY 411 ENNYKTPPVLDSDG--SFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSL 467
 DB 336 REKYLTVASRQEPSTGTTFAVTSILRVAEDWKGDFTSCWVGHEALPLAFTQKTIDRL 395
 QY 468 PGK 470
 DB 396 AGK 398
 RESULT 14
 Q9Y298 PRELIMINARY; PRT; 150 AA.
 ID Q9Y298
 AC Q9Y298
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE IGG VH PROTEIN PRECURSOR (FRAGMENT).
 GN IGG VH.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98322155; PubMed=9657749;
 RA Jacquemin M.G., Vander Elst L.P.L.;
 RT "Mechanism and kinetics of factor VIII inactivation: study with an
 RT IgG4 monoclonal antibody derived from a hemophilia A patient with
 RT inhibitor."
 RC Blood 92:496-506(1998).
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN
 DR EMBL; AJ224083; CAAL1829.1; -.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; Igv; 1.
 KW Signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT NON_TER 150 150
 SQ SEQUENCE 150 AA; 16031 MW; 563D164AB22802D5 CRC64;

Yu, Misook

To: STIC-Biotech/ChemLib
Subject: 09/499,662

Please search SEQ ID:107 and 117. Thanks.

Examiner Misook Yu, Ph.D.
703-308-2454 (Phone)
Art Unit 1642
CM1-8E18 (Room)
CM1-8E12 (Mail Box)

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Thu Apr 25 16:38:28 2002

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 25, 2002, 16:37:14 ; Search time 0.01 Seconds
(without alignments)
0.335 Million cell updates/sec

Title: us-09-499-662-1
Perfect score: 59
Sequence: 1 RTQNTKCRCK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 335 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : aaa63174.genpept.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	335	1	AAA63174

ALIGNMENTS

RESULT 1
AAA63174

Query Match 100.0%; Score 59; DB 1; Length 335;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10

Db 121 RTQNTKCRCK 130

→ 367

Search completed: April 25, 2002, 16:37:14
Job time: 0 sec

extracellular domain

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Schreiber, David

From: Yu, Misook
Sent: Wednesday, March 26, 2003 8:55 AM
To: Schreiber, David
Subject: 09/499,662

David, would you please do interferences search only for following proteins. All of them are small proteins. The case is due this biweek.

1. a single protein sequence: X(any 18-32 aa)-SEQ ID NO:2-X(any 14 aa)-SEQ ID NO:3-X(any 32 aa)-SEQ ID NO:4-X(any 11 aa).
2. a single protein sequence: X(any 23 aa)-SEQ ID NO:5-X(any 15 aa)-SEQ ID NO:6-X(any 32 aa)-SEQ ID NO:7-X(any 10 aa).
3. SEQ ID NOs: 50, 52, 54, 107, 109, 89, 117, 143, 145, 147, 157, 107, 127, 129, 131

Examiner Misook Yu, Ph.D.
703-308-2454 (Phone)
Art Unit 1642
CM1-8E18 (Room)
CM1-8E12 (Mail Box)

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09/499,662

Your SELECT statement is:

s hfe7a

Items File

8 5: Biosis Previews(R)_1969-2002/Apr W3
6 34: SciSearch(R) Cited Ref Sci_1990-2002/Apr W3
4 71: ELSEVIER BIOBASE_1994-2002/Apr W3
3 73: EMBASE_1974-2002/Apr W3
3 94: JICST-EPlus_1985-2002/Mar W2
2 144: Pascal_1973-2002/Apr W3
4 155: MEDLINE(R)_1966-2002/Apr W3
2 156: ToxFile_1966-2002/Feb W4
1 159: Cancerlit_1975-2002/Mar
1 172: EMBASE Alert_2002/Apr W3
7 399: CA SEARCH(R)_1967-2002/UD=13617

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File 5:Biosis Previews(R) 1969-2002/Apr W3

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RANK charge added; see HELP RATES 399.

File 34:SciSearch(R) Cited Ref Sci 1990-2002/Apr W3

(c) 2002 Inst for Sci Info

File 155:MEDLINE(R) 1966-2002/Apr W3

Set Items Description

S1 25 HFE7A

S2 12 RD (unique items)

136052721 CA: 136(4)52721g PATENT

The medicine which contains the human conversion anti- Fas antibody.

INVENTOR(AUTHOR): Serizawa, Nobuki; Haruyama, Hideyuki; Nakahara, Kaori;

Tamaki, Ikuko

LOCATION: Japan,

ASSIGNEE: Sankyo Co., Ltd.

PATENT: Japan Kokai Tokkyo Koho ; JP 2001342148 A2 DATE: 20011211

APPLICATION: JP 200193106 (20010328) *JP 200090918 (20000329)

PAGES: 194 pp. CODEN: JKXXAF LANGUAGE: Japanese CLASS: A61K-039/395A;

A61K-038/00B; A61P-001/16B; A61P-007/06B; A61P-009/00B; A61P-009/10B;

A61P-013/12B; A61P-019/02B; A61P-029/00B; A61P-037/00B; A61P-037/06B;

Set Items Description

S1 25 HFE7A

S2 12 RD (unique items)

S3 3682 ANTI(W)FAS

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09/499, 662

2/9/6

DIALOG(R) File 155:MEDLINE(R)

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13268098 21926856 PMID: 11929798

Murine acute graft-versus-host disease can be prevented by depletion of alloreactive T lymphocytes using activation-induced cell death.

Hartwig Udo F; Robbers Michael; Wickenhauser Claudia; Huber Christoph
Division of Hematology, III Department of Medicine, University Medical
School Mainz, Germany. uhartwig@mail.uni-mainz.de

Blood (United States) Apr 15 2002, 99 (8) p3041-9, ISSN 0006-4971

Journal Code: 7603509

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

Subfile: AIM; INDEX MEDICUS

Depletion of T lymphocytes from allogeneic bone marrow transplants successfully prevents the development of graft-versus-host disease (GvHD) but is associated with impaired engraftment, immunosuppression, and abrogation of the graft-versus-leukemia effect. We therefore explored the possibility of selectively eliminating alloreactive T cells by CD95/CD95L-mediated activation-induced cell death (AICD) in a major histocompatibility complex allogeneic murine model system. Activation of resting or preactivated T lymphocytes from C3H / HeJ (H-2(k)) mice was induced with irradiated BALB/cJ (H-2(d)) mouse-derived stimulators. Substantial decrease (> or = 80%) of proliferative and lytic responses by activated alloreactive T cells was subsequently achieved by incubating the mixed lymphocyte culture with an agonistic monoclonal antibody to CD95, and residual T cells recovered did not elicit alloreactivity upon challenge to H-2(d). Depletion of alloreactive T lymphocytes by AICD was specific because reactivity to an I-A(d)-restricted ovalbumin (OVA) peptide by OVA-specific CD4(+) T cells mixed into the allogeneic T - cell pool and subjected to induction of AICD in the absence of OVA peptide could be preserved. Adoptive transfer of donor-derived allogeneic T lymphocytes, depleted from alloreactive T cells by AICD in vitro, in the parent (C3H/He) to F(1) (C3H/He x BALB/c) GvHD model prevented lethal GvHD. The results presented suggest that alloreactive T cells can effectively be depleted from allogeneic T cells by induction of AICD to prevent GvHD and might introduce a new strategy for the separation of GvH-reactive T cells and T cells mediating antiviral and possibly graft-versus-leukemia effects.

Set	Items	Description
S1	2554	C3H(W)HEJ
S2	384	S1 AND T(W)CELL?

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DIALOG(R) File 5: Biosis Previews(R)
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Regulation of apoptosis and T cell activation by Fas -specific mAb.

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ABSTRACT: **Fas** was initially described as a molecule expressed on the surface of certain cell lines that could mediate programmed cell death (apoptosis) subsequent to ligation by specific mAb. To determine whether mAb to other epitopes on the **Fas** molecule might mediate other functions, we generated a panel of mAb to the extracellular portion of human **Fas**. Significant lysis of **Fas**-expressing target cells was only observed when the new mAb were first bound to a solid-phase support and not when the mAb were added in solution. However, several of these mAb inhibited the killing of target cells induced by the prototypic **Fas**-specific mAb, CH-11. Those mAb that inhibited apoptosis of target cells mediated by the **CH - 11 mAb** also blocked lysis of target cells mediated by cells expressing **Fas** ligand. Finally, some of the **Fas**-specific mAb were found to co-stimulate proliferation of peripheral blood T cells in the presence of immobilized CD3 mAb. Thus, the data indicate the existence of a complex set of interactions mediated by **Fas** in both normal and transformed lymphoid cells that may have important implications regarding the role(s) of this molecule in regulation of immune responses.

Set	Items	Description
S1	12	CH(W)11(W)MAB AND FAS
S2	4	RD (unique items)

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WEST Search History

DATE: Friday, August 30, 2002

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result set

DB=USPT; PLUR=YES; OP=OR

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L19	L15 and frem bp	42949	L19
L18	L14 and hfe7a	0	L18
L17	L11	0	L17
L16	L12 and cd-95	0	L16
L15	L11 and epitopes	0	L15
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L1	(anti-fas) AnD (((@pd > 20020425)!))	12	L1

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